

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 03:18:36 ; Search time 1761 Seconds
(without alignments)

1238.208 Million cell updates/sec

Title: US-10-614-934-14

Perfect score: 266

Sequence: 1 MIFCQKQKINVRNNSGE.....IRIYNTRAKCINIKCNCYP 45

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Database: GenEmbl:*

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2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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9: gb_pr:*
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11: gb_srs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	266	100.0	138	6	AR359345
2	102	38.3	151	12	SYNCTX
3	101	38.0	114	6	AR359343
4	92.5	34.8	186	6	AX063238

5	91.5	34.4	154	6	118309	118309 Sequence 5
6	91.5	34.0	254	3	AAU427744	AAU427744 Androcton
7	90.5	34.0	254	3	AAU427743	AAU427743 Androcton
8	90	33.8	323	3	AF225782	AF225782 Opisthot
9	88	33.1	288	3	AF151537	AF151537 Butus ma
10	88	33.1	348	3	AF247058	AF247058 Butus ma
11	88	33.1	372	3	AF208300	AF208300 Butus ma
12	87.5	32.9	180	6	AX063240	AX063240 Sequence
13	86.5	32.5	120	6	118306	118306 Sequence 2
14	86.5	32.5	174	6	AX063254	AX063254 Sequence
15	86.5	32.5	263	3	AAU427745	AAU427745 Androcton
16	83.5	31.4	313	3	AF079062	AF079062 Mesobutn
17	83.5	31.4	400	3	AF208298	AF208298 Butus ma
18	82	30.8	160	3	PIU79579	PIU79579 Pandinus im
19	79.5	29.9	300	3	AF153692	AF153692 Mesobutn
20	79.5	29.9	190371	2	AC116830	AC116830 Mus muscu
21	78.5	29.5	281	3	AF541980	AF541980 Butus ma
22	78	29.3	180	6	AR359346	AR359346 Sequence
23	77.5	29.1	293	3	AY156725	AY156725 Mesobutn
24	77	28.9	150	6	AR359344	AR359344 Sequence
25	76.5	28.8	379	3	AF208299	AF208299 Butus ma
26	75	28.2	176	6	AX063250	AX063250 Sequence
27	75	28.2	181329	2	BX569779	BX569779 Dantio rer
28	73	27.4	177	6	AR359339	AR359339 Sequence
29	73	27.4	312	3	AY225783	AY225783 Opisthot
30	72.5	27.3	110000	2	AC098036	AC098036 Continuation (3 of
31	72.5	27.3	213887	2	AC128587	AC128587 Rattus no
32	72.5	27.3	239732	2	AC098491	AC098491 Rattus no
33	72.5	27.3	322972	2	AC129853	AC129853 Rattus no
34	72	27.1	4674	3	PTG11A2	PTG11A2 X96468 P.tetraul
35	72	27.1	36596	2	AC149403	AC149403 Phakopsor
36	72	27.1	151441	2	AC149687	AC149687 Bos tauru
37	72	27.1	238844	2	AC097683	AC097683 Rattus no
38	71.5	26.9	272	3	S74733	S74733 KMTX2-Rallot
39	71.5	26.9	183629	2	CR847835	CR847835 Dantio rer
40	71.5	26.9	185257	5	AL929558	AL929558 Zebrafish
41	71.5	26.9	209810	2	AC106935	AC106935 Rattus no
42	71.5	26.9	214878	2	CR846099	CR846099 Dantio rer
43	71	26.7	177	6	AX063252	AX063252 Sequence
44	71	26.7	144641	2	AC116530	AC116530 Mus muscu
45	71	26.7	146202	10	AL928553	AL928553 Mouse DNA

ALIGNMENTS

RESULT 1
AR359345
LOCUS AR359345 138 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 13 from patent US 6593141.
ACCESSION AR359345
VERSION AR359345.1 GI:33765592
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 138)
AUTHORS Herman,R., Wong,J.F., Lu,A.L., Presnail,J.K. and Lee,J.-M.
TITLE Scorpion toxins
JOURNAL Patent: US 6593141-A 13 15-JUL-2003;
FEATURES
source location/Qualifiers
1..138
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores: 6.62e-26 Length: 138
Pred. No.: 266.00 Matches: 45
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

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US-10-614-934-14 (1-45) x AR359345 (1-138)

QY 1 MetMec1lePheCySGInGlyGlnLysIleAsnTYrArgCySaAsnSergIyGlu 20
DB 1 ATGATGATTTTCTGCAAGCCAGAAAAATAATTTCATGTATTAATAGCGGTAG 60

QY 21 CysIleProHisCysIleArgIleTYrAsnThrArgAlaIalysCysIleAsnLysThr 40
DB 61 TGAATTCACATTCATCAGAAATATATACACAGAGACGAAAGTATTATTAATAACA 120

QY 41 CysAsnCysTYrPro 45
DB 121 TGCATTTGTTATCCA 135

RESULT 2
SYNCTX 151 bp DNA linear SYN 27-APR-1993
LOCUS Synthetic scorpion charybdotoxin gene,3' end.
DEFINITION M64610
ACCESSION M64610
VERSION M64610.1 GI:208160
KEYWORDS charybdotoxin; peptide blocker of K+ channels.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 151)
AUTHORS Park,C.S., Hausdorff,S.F. and Miller,C.
TITLE Design, synthesis, and functional expression of a gene for
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (6), 2046-2050 (1991)
MEDLINE 91172749
PUBMED 1706515
COMMENT Original source text: Synthetic DNA.
FEATURES
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        1..151
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /gene="CTX"
            /gene="CTX"
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            /codon_start=1
            /transl_table=1
            /product="charybdotoxin"
            /protein_id="AAV3014.1"
            /db_xref="GI:208161"
            /translation="VDSIEGRQPTNVSCTTSKECWEVCQRLHNTSRGKMKKRCRY
S"

ORIGIN
Alignment Scores:
Pred. No.: 0.000188 Length: 151
Score: 102.00 Matches: 17
Percent Similarity: 58.97% Conservative: 6
Best Local Similarity: 43.59% Mismatches: 16
Query Match: 38.35% Indels: 0
DB: 12 Gaps: 0

US-10-614-934-14 (1-45) x SYNCTX (1-151)

QY 6 GlnGlyGlnLysLysIleAsnTYrArgCySaAsnSergIyGluCysIleProHisCys 25
DB 16 GAAGGTGCTCAATTACCAATGTTCTTGACCACTTCTAAGGAATGTGGTCCGTTGT 75

QY 26 IleArgIleTYrAsnThrArgAlaIalysCysIleAsnLysThrCysAsnCysTYr 44
DB 76 CAACGCTGCTCAACACACGCGCGTAAATGCAATGAACAAAAATGTCGTTTAC 132

RESULT 3
LOCUS AR359343
DEFINITION Sequence 9 from patent US 6593141.
ACCESSION AR359343

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VERSION AR359343.1 GI:33765590
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 114)
AUTHORS Herman,R., Wong,J.F., Lu,A.L., Prenatal,J.K. and Lee,J.-M.
TITLE Scorpion toxins
JOURNAL Patent: US 6593141-A 9 15-JUL-2003;
FEATURES
    source
        1..114
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 0.00019 Length: 114
Score: 101.00 Matches: 17
Percent Similarity: 58.82% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 14
Query Match: 37.97% Indels: 0
DB: 6 Gaps: 0

US-10-614-934-14 (1-45) x AR359343 (1-114)

QY 12 AsnTYrArgCySaAsnSergIyGluCysIleProHisCysIleArgIleTYrAsnThr 31
DB 10 AATGTGCGCGTGAAGATTCGGAACAATGTCGTCAGTTTGCAATAAAGATTAATAT 69

QY 32 ArgAlaIalysCysIleAsnLysThrCysAsnCysTYrPro 45
DB 70 AATGCGGAAGTGTGTAATGACAAATGTAATTTGTTATCCA 111

RESULT 4
LOCUS AX063238
DEFINITION Sequence 3 from Patent WO0078958.
ACCESSION AX063238
VERSION AX063238.1 GI:12541063
KEYWORDS
SOURCE Hotentocota judaica
ORGANISM Hotentocota judaica
REFERENCE 1
AUTHORS Hermann,R., Lee,J.M. and Wong,J.F.
TITLE Scorpion toxins from buthous judaicus
JOURNAL Patent: WO 0078958-A 3 28-DEC-2000;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
    source
        1..186
            /organism="Hotentocota judaica"
            /mol_type="unassigned DNA"
            /db_xref="taxon:6863"

ORIGIN
Alignment Scores:
Pred. No.: 0.00407 Length: 186
Score: 92.50 Matches: 17
Percent Similarity: 50.00% Conservative: 6
Best Local Similarity: 36.96% Mismatches: 22
Query Match: 34.77% Indels: 1
DB: 6 Gaps: 1

US-10-614-934-14 (1-45) x AX063238 (1-186)

QY 1 MetMec1lePheCySGInGlyGlnLysIleAsnTYrArgCys---AsnAsnSergIy 19
DB 46 ATGCTTAATTCGAGCACCGCTCAATACAGATTGATGTAACGTATGAGGAGAGACAT 105

QY 20 GluCysIleProHisCysIleArgIleTYrAsnThrArgAlaIalysCysIleAsnLys 39
DB 106 AATTGCGTAACCACTGATGATTAATACGGACACCACTAAACTTAATGCAATCAACGAT 165

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Qy 40 ThrCysAenCysTyrPro 45
 Db 166 CGGTCCACTGTATCCG 183
 RESULT 5
 LOCUS 118309 154 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 5 from patent US 5494895.
 ACCESSION 118309
 VERSION 118309.1 GI:1598664
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 154)
 AUTHORS Garcia,M.L., Koo,G.C., Leonard,R.J., Lin,C.-C.S., Slaughter,R.S.,
 Stevens,S.P. and Williams,J.M.
 TITLE Scorpion peptide margatoxin with immunosuppressant activity
 JOURNAL Patent: US 5494895-A 5 27-FEB-1996;
 FEATURES Location/Qualifiers
 source 1..154
 /organism="Unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.00452 Length: 154
 Score: 91.50 Matches: 16
 Percent Similarity: 58.54% Conservative: 8
 Best Local Similarity: 39.02% Mismatches: 16
 Query Match: 34.40% Indels: 1
 DB: 6 Gaps: 1
 US-10-614-934-14 (1-45) x 118309 (1-154)
 Qy 6 GlnGlnGlnLysLysLysLeuTyrArgCysAenAenSergLysCysLeuProHisCys 25
 Db 16 GAGGTCTGACATCATCACTTAATGACACTCTCCGAACACAGTGCCTGCCGCGTC 75
 Qy 26 IleArgIleTyrAsnThrArgAla--AlaLysCysIleAsnLysThrCysAenCysTyr 44
 Db 76 AAGCTCAGTTCGTCAGTCTGCTGCTAATGATGATGACGTAATGCAATGCTAC 135
 Qy 45 Pro 45
 Db 136 CCG 138
 RESULT 6
 LOCUS AAU427744 254 bp mRNA linear INV 10-JAN-2003
 DEFINITION Androctonus australis partial mRNA for toxin AaTx2.
 ACCESSION AJ427744
 VERSION AJ427744.1 GI:27652633
 KEYWORDS toxin AaTx2.
 ANDROCTONUS AUSTRALIS (Sahara scorpion)
 ANDROCTONUS AUSTRALIS
 EUKARYOTA; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 Butiidae; Butioidae; Butiidae; Androctonus.
 REFERENCE 1
 AUTHORS Vacher,H., Alami,M., Legros,C., Possani,L.D., Bougis,P.E. and
 Martin-Baucalire,M.F.
 TITLE Novel toxins blocking A-type potassium currents: purification from
 venoms of diverse Androctonus species, amino acid sequence
 determination, pharmacological characterisation and gene structure
 Unpublished
 JOURNAL 2 (bases 1 to 254)
 REFERENCE Martin-Baucalire,M.F.
 AUTHORS Direct Submission
 TITLE Submitted (10-JAN-2002) Martin-Baucalire M.F., Institut Jean Roche,
 UMR 6560 CNRS Université de la Méditerranée, Bd Pierre Dramard,
 F-13916 Marseille cedex 20, FRANCE
 FEATURES Location/Qualifiers

source 1..254
 /organism="Androctonus australis"
 /mol_type="mRNA"
 /db_xref="taxon:6858"
 /clone="pcd-3x9"
 /country="Tunisia:Beni-Khedache"
 <18..197
 /codon_start=1
 /product="toxin AaTx2"
 /protein_id="CAD20743.1"
 /db_xref="GI:27652633"
 /translation="MKFSSITLLTLTLCMSIFGNCQVETNNKCGGSCASVCRVIG
 VAAGKINRCVCYP"
 sig_peptide 18..83
 mat_peptide 84..192
 /product="toxin AaTx2"
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 Alignment Scores:
 Pred. No.: 0.0076 Length: 254
 Score: 91.50 Matches: 19
 Percent Similarity: 48.89% Conservative: 3
 Best Local Similarity: 42.22% Mismatches: 22
 Query Match: 34.40% Indels: 1
 DB: 3 Gaps: 1
 US-10-614-934-14 (1-45) x AAU427744 (1-254)
 Qy 1 MetMetIlePheCysGlnGlnLysIleAsnTyrArgCysAenSergLysIle 20
 Db 63 ATGACATCTTCGCGCAATGCGCAAGTGAACCAAGAAATGT---CAAGGTGATCG 119
 Qy 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaIleLysCysIleAsnLysThr 40
 Db 120 TGTGCTTAGTATGAGAGATATGAGATGAGTCTGCTGCGCAATGATATATGGAACA 179
 Qy 41 CysAenCysTyrPro 45
 Db 180 TGTGCTCTGATCCCC 194
 RESULT 7
 LOCUS AAU427743 254 bp mRNA linear INV 10-JAN-2003
 DEFINITION Androctonus australis partial mRNA for toxin AaTx1.
 ACCESSION AJ427743
 VERSION AJ427743.1 GI:27652631
 KEYWORDS toxin AaTx1.
 ANDROCTONUS AUSTRALIS (Sahara scorpion)
 ANDROCTONUS AUSTRALIS
 EUKARYOTA; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 Butiidae; Butioidae; Butiidae; Androctonus.
 REFERENCE 1
 AUTHORS Vacher,H., Alami,M., Legros,C., Possani,L.D., Bougis,P.E. and
 Martin-Baucalire,M.F.
 TITLE Novel toxins blocking A-type potassium currents: purification from
 venoms of diverse Androctonus species, amino acid sequence
 determination, pharmacological characterisation and gene structure
 Unpublished
 JOURNAL 2 (bases 1 to 254)
 REFERENCE Martin-Baucalire,M.F.
 AUTHORS Direct Submission
 TITLE Submitted (10-JAN-2002) Martin-Baucalire M.F., Institut Jean Roche,
 UMR 6560 CNRS Université de la Méditerranée, Bd Pierre Dramard,
 F-13916 Marseille cedex 20, FRANCE
 FEATURES Location/Qualifiers
 source 1..254
 /organism="Androctonus australis"
 /mol_type="mRNA"
 /db_xref="taxon:6858"
 /clone="pcd-3x11"
 /country="Tunisia:Beni-Khedache"
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 /codon_start=1

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ORIGIN
sig_peptide      /product="toxin AtTx1"
mat_peptide      /protein_id="CAD20742.1"
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                  18 . 83
                  84 . 192
                  /product="toxin AtTx1"

ALIGNMENT SCORES:
Pred. No.:      0.0103      Length:      254
Score:          90.50      Matches:      19
Percent Similarity: 48.89%      Conservative: 3
Best Local Similarity: 42.22%      Mismatches: 22
Query Match:    34.02%      Indels:      1
DB:              3      Gaps:      1

US-10-614-934-14 (1-45) x AMU427743 (1-254)

QY      1 MetMetIlePheCysGlnGlyGlnLysIleAsnTyrArgCysAsnAsnSerGlyGlu 20
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      63 ATGAGCATCTTCGGCAATTGCCAATTGAAACAAACAGAAATGT---CAAGTGTGATCG 119

QY      21 CysIlePheHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      120 TGTGCTTCAGTATGTAGAGATTAATGTGAGTACGCTGCGCAATGTATTATGGAAGA 179

QY      41 CysAsnCysTyrPro 45
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      180 TGTGCTGCTACCCC 194

RESULT 8
AY225782      323 bp mRNA linear INV 12-OCT-2003
LOCUS      Opisthophthalmus carinatus potassium channel toxin KTx4 mRNA,
DEFINITION      complete cds.
ACCESSION      AY225782
VERSION      AY225782.1 GI:37539451
KEYWORDS
SOURCE      Opisthophthalmus carinatus
ORGANISM      Opisthophthalmus carinatus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Iurida; Scorpionioidea; Scorpionidae; Scorpioninae; Opisthophthalmus.
REFERENCE      1 (bases 1 to 323)
AUTHORS      Zhu,S., Isabelle,H., Dyason,K., Verdonck,F. and Tytgat,J.
TITLE      Evolutionary trace analysis of scorpion toxins specific for
            K-channels
JOURNAL      Proteins (2003) In press
REFERENCE      2 (bases 1 to 323)
AUTHORS      Zhu,S., Dyason,K., Verdonck,F. and Tytgat,J.
TITLE      Scorpion alpha-K+ Channel Toxin Family: Molecular Cloning and
            Evolutionary Prediction of Channel-Binding Sites
JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 323)
AUTHORS      Tytgat,J., Zhu,S., Verdonck,F. and Dyason,K.
TITLE      Direct Submission
JOURNAL      Submitted (25-JAN-2003) Lab of Toxicology, Leuven University, E.
            Van Evenenraat 4, Leuven 3000, Belgium
FEATURES
            source
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            /organism="Opisthophthalmus carinatus"
            /mol_type="mRNA"
            /db_xref="taxon:190115"
            /tissue_type="venom gland"
            31..216
            /note="OckTx4; belongs to alpha-potassium channel toxin
            subfamily 6"
            /codon_start=1
            /product="potassium channel toxin KTx4"
            /protein_id="AAP73820.1"
            /db_xref="GI:37539452"
            /translation="MNAKFILLLVTTTLLPDAKGAETIRCSGTRECYAPCQKLTG

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ORIGIN
CLNAKCMNRKACKYCV"

ALIGNMENT SCORES:
Pred. No.:      0.0153      Length:      323
Score:          90.00      Matches:      17
Percent Similarity: 60.98%      Conservative: 8
Best Local Similarity: 41.46%      Mismatches: 13
Query Match:    33.83%      Indels:      3
DB:              3      Gaps:      1

US-10-614-934-14 (1-45) x AY225782 (1-323)

QY      5 CysGlnGlyGlnLysLysIleAsnTyr-ArgCysAsnAsnSerGlyGlyCysIleProhi 24
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      90 TGCAAGAGGCGCCGCA-----AATTATCAGATGAGTGAACAAAGGAGTGTATGCCCC 143

QY      24 CysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThrCysAsnCysTyr 44
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      144 ATGCCAAGAAGCTTACCGAGTCTTTAATGCMAAATGATGAACAAAGCCTGCAATGTTA 203

QY      44 T 44
        ||
Db      204 C 204

RESULT 9
AF151537      288 bp mRNA linear INV 18-AUG-2003
LOCUS      Butus martenisi potassium channel toxin precursor (Tx2) mRNA,
DEFINITION      complete cds.
ACCESSION      AF151537
VERSION      AF151537.1 GI:3337896
KEYWORDS
SOURCE      Mesobuthus martenisi (Butus martenisi)
ORGANISM      Mesobuthus martenisi
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Butiida; Butioidae; Butiidae; Mesobuthus.
REFERENCE      1 (bases 1 to 288)
AUTHORS      Zeng,X.-C., Li,W.-X. and Zu,S.-Y.
TITLE      The cDNA sequence encoding the precursor of toxin TX2 from the
            Chinese scorpion Butus martenisi Karsch which is active on
            potassium channel
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 288)
AUTHORS      Li,W.-X., Zeng,X.-C. and Zu,S.-Y.
TITLE      Direct Submission
JOURNAL      Submitted (14-MAY-1999) Department of Virology and Molecular
            Biology, Institute of Virology, Wuhan University, Luojia Street,
            Wuhan, Hubei 430072, P.R. China
FEATURES
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            /mol_type="mRNA"
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            /tissue_type="venom gland"
            /note="authorily: Butus martenisi Karsch"
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            /gene="Tx2"
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            /codon_start=1
            /product="potassium channel toxin precursor"
            /protein_id="AAQ13576.1"
            /db_xref="GI:3337897"
            /translation="MKISFLLLAIVICISGITEAOPTNVSCASGQCPVCKLFGT
            YRGKMSKRCIS"
ORIGIN

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Qy 32 ArgAlaAlaLysCysIleAsnLysThrCysAsnCysTyr 44
Db 259 TACAGGGGAAATGTATGATAATGTAATGCGCTGTGTAT 297

RESULT 12
AX063240

LOCUS AX063240 180 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 5 from Patent WO0078958.
ACCESSION AX063240
VERSION AX063240.1 GI:12541064
KEYWORDS
SOURCE Hottentotta judaica
ORGANISM Hottentotta judaica
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Butrida; Buthidae; Buthidae; Hottentotta.

REFERENCE
1 Herrmann, R., Lee, J.M. and Wong, J.F.
AUTHORS Scorpion toxins from buthoidus judaicus
TITLE Patent: WO 0078958-A 5 28-DEC-2000;
JOURNAL E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
source Location/Qualifiers
1..180
/organism="Hottentotta judaica"
/mol_type="unassigned DNA"
/db_xref="taxon:6863"

ORIGIN

Alignment Scores:
Pred. No.: 0.0177 Length: 180
Score: 87.50 Matches: 18
Percent Similarity: 46.67% Conservative: 3
Best Local Similarity: 40.00% Mismatches: 23
Query Match: 32.89% Indels: 1
DB: 6 Gaps: 1

US-10-614-934-14 (1-45) x AX063240 (1-180)

Qy 1 MetMetIlePheCysGlnGlyGlnLysIleAsnTyrArgCysAsnAsnSerGlyGlu 20
Db 46 ATGACCAATATGATTAATGTCACCAAGTAGAACAATGCAATGT---ACAGTGCGCTCA 102

Qy 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
Db 103 TGTCTTCACATGATAAAGAGTAATAGAGTACTGACGAGAAATGCAATTAATGAGA 162

Qy 41 CysAsnCysTyrPro 45
Db 163 TGTGTCTGCTATCCG 177

RESULT 13
118306
LOCUS 118306 120 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 2 from patent US 5494895.
ACCESSION 118306
VERSION 118306.1 GI:1598661
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 120)
AUTHORS Garcia, M.L., Koo, G.C., Leonard, R.J., Lin, C.-C.S., Slaughter, R.S.,
Stevens, S.P. and Williamson, J.M.
TITLE Scorpion peptide margatoxin with immunosuppressant activity
JOURNAL Patent: US 5494895-A 2 27-FEB-1996;
FEATURES
source Location/Qualifiers
1..120
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.0157 Length: 120
Score: 86.50 Matches: 15

Percent Similarity: 58.33% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 14
Query Match: 32.52% Indels: 1
DB: 6 Gaps: 1

US-10-614-934-14 (1-45) x 118306 (1-120)

Qy 11 IleAsnTyrArgCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsn 30
Db 7 ATCAAGCTTAATGACACCTCTCCGAAACAGTGCCTGCCGTCGCAAGTCAGTCCGT 66

Qy 31 ThrArgAla---AlaLysCysIleAsnLysThrCysAsnCysTyrPro 45
Db 67 CAGTCTGTGTGTCTTAATGATGTAAGCAAGTAAATGCAAAATGTAACCG 114

RESULT 14
AX063254
LOCUS AX063254 174 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 19 from Patent WO0078958.
ACCESSION AX063254
VERSION AX063254.1 GI:12541071
KEYWORDS
SOURCE Hottentotta judaica
ORGANISM Hottentotta judaica
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Butrida; Buthidae; Buthidae; Hottentotta.

REFERENCE
1 Herrmann, R., Lee, J.M. and Wong, J.F.
AUTHORS Scorpion toxins from buthoidus judaicus
TITLE Patent: WO 0078958-A 19 28-DEC-2000;
JOURNAL E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
source Location/Qualifiers
1..174
/organism="Hottentotta judaica"
/mol_type="unassigned DNA"
/db_xref="taxon:6863"

ORIGIN
unsure 9
unsure 88

Alignment Scores:
Pred. No.: 0.0231 Length: 174
Score: 86.50 Matches: 17
Percent Similarity: 52.27% Conservative: 6
Best Local Similarity: 38.64% Mismatches: 20
Query Match: 32.52% Indels: 1
DB: 6 Gaps: 1

US-10-614-934-14 (1-45) x AX063254 (1-174)

Qy 1 MetMetIlePheCysGlnGlyGlnLysIleAsnTyrArgCysAsnAsnSerGlyGlu 20
Db 40 ATATATGATTTTCAACCGAAGCTCAG---TTTATGACGTGAATGCACATCATTAAAGAA 96

Qy 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
Db 97 TGTGGGCTTATTTGTATGAGAAGATTGTGTGGCCAGAGAAATGTCATTAATTAACAA 156

Qy 41 CysAsnCysTyr 44
Db 157 TGCCGTGTGTAT 168

RESULT 15
AAU427745
LOCUS AAU427745 263 bp DNA linear INV 10-JAN-2003
DEFINITION Androctonus australis tx1 gene for toxin AaTx1, exons 1-2.
ACCESSION AAU427745
VERSION AAU427745.1 GI:27652635
KEYWORDS toxin AaTx1, tx1 gene.
SOURCE Androctonus australis (Sahara scorpion)
ORGANISM Androctonus australis
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Butrida; Buthidae; Buthidae; Androctonus.

REFERENCE 1
 Vacher, H., Alami, M., Legros, C., Possani, L.D., Bougis, P.E. and

AUTHORS Martin-Eaucalade, M.F.

TITLE Novel toxins blocking A-type potassium currents: purification from
 venoms of diverse Androctonus species, amino acid sequence
 determination, pharmacological characterisation and gene structure

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 263)
 AUTHORS Martin-Eaucalade, M.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2002) Martin-Eaucalade M.F., Université de la
 Méditerranée, Institut Jean Roche UMR 6560 CNRS, Bd Pierre Dramard,
 F-13916 Marseille cedex 20, FRANCE

FEATURES
 source 1..263
 location/Qualifiers

/organism="Androctonus australis"

/mol_type="genomic DNA"

/db_xref="taxon:6858"

/tissue_type="muscle"

/country="Tunisia:Beni-Khadache"

1..263

/gene="tx1"

join(1..66,133..263)

/gene="tx1"

1..66

/gene="tx1"

/number=1

join(18..66,133..263)

/gene="tx1"

/codon_start=1

/product="toxin AaTx1"

/protein_id="CAD20744.1"

/db_xref="GI:27652636"

/translation="MKFSSIIITLILICMSLFGNCQIETNKKCGGSCASVCRRVIG
 VAAKCIINGRCVCYP"

join(18..66,133..149)

/gene="tx1"

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/gene="tx1"

/product="toxin AaTx1"

67..132

/gene="tx1"

/number=1

133..263

/gene="tx1"

/number=2

sig_peptide
 mat_peptide
 intron
 exon

ORIGIN

Alignment Scores:

Pred. No.:	0.0354	Length:	263
Score:	86.50	Matches:	18
Percent Similarity:	48.84%	Conservative:	3
Best Local Similarity:	41.86%	Mismatches:	21
Query Match:	32.52%	Indels:	1
DB:	3	Gaps:	1

US-10-614-934-14 (1-45) x ANU427745 (1-263)

QY	3	11epheCysGInGlyGlnLysLeuLeuTyrArgCysAsnAsnSerGlyGlnCysIle	22
Db	135	ATCTTCGGCAATTGCCAATTGAACAACAAGAAATGT---CAAGTGGATCGTGTCT	191
QY	23	ProHisCysIleArgGIIeTyrAsnThrArgAlaAlaLysCysIleAsnLysThrCysAsn	42
Db	192	TCAGTATGTAGAGAGATATGAGTACGTCTGGCAAAATGATTAATGAAGAAGATGTCT	251
QY	43	CysTyrPro	45
Db	252	TGCTACCCC	260

Search completed: August 19, 2005, 05:41:25
 Job time : 1765 secs

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XX  Herrman R, Wong JF, Lu AL, Presnail JK, Lee J;
PI  WPI: 2000-422976/36.
DR  P-PSDB: AAY99579.
XX
PT  New nucleic acid fragment encoding a scorpion toxin that is a potassium
PT  channel agonist, useful for creating transgenic plants that are more
XX  insect-tolerant.
XX
PS  Claim 2; Page 41; 44pp; English.
XX
CC  The present sequence encodes the scorpion potassium channel agonist
CC  Charybotoxin. The toxin forms a compact structure kept rigid by three
CC  disulphide bonds. Potassium channels modulate a number of cellular events
CC  such as muscle contraction, neuro-endocrine secretion, frequency and
CC  duration of action potentials, electrolyte homeostasis and resting
CC  membrane potential. The agonist has a high affinity for the channel and
CC  may therefore act by producing an irreversible blockade of the channel.
CC  The nucleotide sequence was isolated from clone 1st.pK0016.c8.f of a cDNA
CC  library representing mRNAs from Leiurus scorpion telson tissues. The toxin
CC  is insecticidal and the cDNA sequence can therefore be used to create
CC  transgenic plants that express the toxin as a means of insect pest
CC  control. The amino acid sequence of the present toxin shows homology to
CC  the Charybotoxin artificial sequence (AAY99587)
XX
SQ  Sequence 138 BP; 55 A; 21 C; 24 G; 38 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          7.83e-27      Length:      138
Score:             266.00         Matches:      45
Percent Similarity: 100.00%       Conservative: 0
Best Local Similarity: 100.00%    Mismatches:  0
Query Match:       100.00%        Indels:      0
DB:                3             Gaps:        0

US-10-614-934-14 (1-45) x AAA48436 (1-138)

QY  1 MetMetIlePheCySGInGIyGInLySileAsnTYrArGYSAsnAsnSerGIyGlu 20
Db  1 ATGATGAAATTTCTGCGCAAGGCCAGAAAAAATAATTAATTCATGTAATTAATGCGGTGAG 60
QY  21 CysIleProHisCysIleArgIleTYrAsnThraAlaAlaIyS CysIleAsnLyThr 40
Db  61 TGTATTCACATGTCATCAGATATATATACACACAGACAGCAAGTGTATTAATAAAAAACA 120
QY  41 CysAsnCYsTYrPro 45
Db  121 TGCAAATGTATATCCA 135

RESULT 2
AAA48434
ID  AAA48434 standard; cDNA; 114 BP.
XX
AC  AAA48434;
XX
DT  15-SEP-2000 (first entry)
XX
DE  Scorpion potassium channel agonist Tityustoxin k Alpha cDNA.
XX
KW  Scorpion; tityustoxin k alpha; potassium channel agonist; insecticidal;
KW  insect-tolerant transgenic plant; ss.
XX
OS  Leiurus quinquestratus.
XX
FH  Key Location/Qualifiers
FT  CDS 1..114
FT  CDS /*tag= a
FT  CDS /partial
FT  CDS /product= "Tityustoxin k Alpha"
XX
XX  WO200032777-A2.
XX

```

```

PD  08-JUN-2000.
XX
XX  Herrman R, Wong JF, Lu AL, Presnail JK, Lee J;
PF  WPI: 2000-422976/36.
XX  P-PSDB: AAY99577.
XX
DR  WPI: 2000-422976/36.
XX
XX  New nucleic acid fragment encoding a scorpion toxin that is a potassium
XX  channel agonist, useful for creating transgenic plants that are more
XX  insect-tolerant.
XX
PS  Claim 2; Page 41; 44pp; English.
XX
CC  The present sequence encodes the scorpion potassium channel agonist
CC  Tityustoxin k Alpha. The toxin forms a compact structure kept rigid by
CC  three disulphide bonds. Potassium channels modulate a number of cellular
CC  events such as muscle contraction, neuro-endocrine secretion, frequency
CC  and duration of action potentials, electrolyte homeostasis and resting
CC  membrane potential. The agonist has a high affinity for the channel and
CC  may therefore act by producing an irreversible blockade of the channel.
CC  The nucleotide sequence was isolated from clone 1st.pK0015.d2.f of a cDNA
CC  library representing mRNAs from Leiurus scorpion telson tissues. The toxin
CC  is insecticidal and the cDNA sequence can therefore be used to create
CC  transgenic plants that express the toxin as a means of insect pest
CC  control. The amino acid sequence of the present toxin shows homology to
XX  the sequence of tityustoxin k alpha from Tityus serrulatus (AAY99585)
XX
SQ  Sequence 114 BP; 44 A; 15 C; 23 G; 32 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          6.55e-05      Length:      114
Score:             101.00         Matches:      17
Percent Similarity: 58.82%       Conservative: 3
Best Local Similarity: 50.00%    Mismatches: 14
Query Match:       37.97%        Indels:      0
DB:                3             Gaps:        0

US-10-614-934-14 (1-45) x AAA48434 (1-114)

QY  12 AsnTYrArGYSAsnAsnSerGIyGluCysIleProHisCysIleArgIleTYrAsnThr 31
Db  10 AATGTGCCGTGCAAGAAATTCGGACAAATGTCGTCACATTGCAATAAAAAGATTAATAT 69
QY  32 ArgAlaAlaIyS CysIleAsnLyS ThrCYsAsnCYsTYrPro 45
Db  70 AATAGCGGAAAGTGTGTAATGACAAATGATTTGTTATCA 111

RESULT 3
AAF27524
ID  AAF27524 standard; DNA; 186 BP.
XX
AC  AAF27524;
XX
DT  28-MAR-2001 (first entry)
XX
DE  Scorpion kaliotoxin 2 precursor DNA.
XX
KW  Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
XX
OS  Hottentotta judaica.
XX
FH  Key Location/Qualifiers
FT  CDS 1..186
FT  CDS /*tag= a
FT  CDS /partial
FT  CDS /product= "kaliotoxin 2 precursor"
XX
XX  21-JUN-2000; 2000WO-US017049.
XX

```


PT New polynucleotides encoding scorpion venom potassium-channel agonist
PT proteins for production e.g. of insect-tolerant transgenic plants for
PT controlling insect pest damage and parasitic worm infections.
XX
PS Claim 1; Page 45; 50pp; English.
XX
CC The present invention relates to scorpion toxins. The invention may be
CC used for the creation of transgenic plants which express K-channel
CC modifiers, useful as a means for controlling insect pests by producing
CC insect-tolerant plants. In the prevention and/or treatment of insect pest
CC damage and parasitic worm infections in animals and humans, the invention
CC may also find use in creating specific new pesticides and antihelmintic
CC drugs that are also non-toxic to humans, pets and livestock
XX
SQ Sequence 180 BP; 59 A; 27 C; 36 G; 58 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.00742 Length: 180
Score: 87.50 Matches: 18
Percent Similarity: 46.67% Conservative: 3
Best Local Similarity: 40.00% Mismatches: 23
Query Match: 32.89% Indels: 1
Gaps: 1
DB:
US-10-614-934-14 (1-45) x AAF27525 (1-180)
Qy 1 MetMetIlePheCysGlnGlyGlnIleValSerIleAsnTyrArgCysAsnAsnSerGlyGlu 20
Db 46 ATGACCAATATGTTATTAATGCGCAATGAAACAAATGGAATGT--ACAGGTGGCTCA 102
Qy 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaIleCysIleAsnIleThr 40
Db 103 TGTGCTTCACATGTAAAGAGATATAGAGTAGCTGCAGAGAAATGATTAATGGAAGA 162
Qy 41 CysAsnCysTyrPro 45
Db 163 TGTGTCTGCTATCCG 177
RESULT 6
AAQ84344
ID AAQ84344 standard; cDNA, 127 BP.
XX
AC AAQ84344;
XX
DT 25-MAR-2003 (revised)
DT 24-AUG-1995 (first entry)
XX
DE Constructed gene encoding scorpion margatoxin (MgTX).
XX
KM Scorpion venom; Centruroides margaritatus; margatoxin; MgTX;
KM synthetic gene; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..117
FT /*tag= a
XX
PN WO9503065-A1.
XX
PD 02-FEB-1995.
XX
PF 19-JUL-1994; 94WO-US008063.
XX
PR 22-JUL-1993; 93US-00096942.
XX
PA (MERI) MERCK & CO INC.
XX
PI Garcia ML, Koo GC, Leonard RJ, Lin C, Slaughter RS, Stevens SP;
PI Williamson JM;
XX
XX WPI; 1995-075021/10.
XX
DR P-PSDB; AAR6876.

XX
XX New purified scorpion venom peptide, Margatoxin - useful as a potent and
PT selective inhibitor of a voltage-dependent potassium channel as an
PT immunosuppressant.
XX
PS Claim 13; Page 31; 42pp; English.
XX
XX Margatoxin (MgTX) is purified to homogeneity from venom of the scorpion
CC C. margaritatus. The gene encoding MgTX is constructed and this gene is
CC expressed in E. coli to produce recombinant MgTX. MgTX is an inhibitor of
CC a voltage-dependent K+ channel present in human lymphocytes. It is useful
CC as an immunosuppressant. MgTX is useful as a selective probe for Kv1.3,
CC and may be employed in a screen for other Kv1.3 inhibitors exhibiting
CC immunosuppressant activity. MgTX inhibits interleukin 2 produ. in human T
CC -lymphocytes (Lin et al., J. Exp. Med. 177, 637, 1993). (updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 127 BP; 35 A; 37 C; 28 G; 27 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.00648 Length: 127
Score: 86.50 Matches: 15
Percent Similarity: 58.33% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 14
Query Match: 32.52% Indels: 1
Gaps: 1
DB:
US-10-614-934-14 (1-45) x AAQ84344 (1-127)
Qy 11 IleAsnTyrArgCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsn 30
Db 7 ATCAACGTTAAATGCACTCTCCGAAACAGTGCCTGCCGCCGCAAGCTCAGTTGGT 66
Qy 31 ThrArgAla--AlaIleCysIleAsnIleThrCysAsnCysTyrPro 45
Db 67 CAGTCTGCTGCTTAATGATGACGTAACGTAATGCAAAATGTAACCG 114
RESULT 7
AAF27532
ID AAF27532 standard; DNA, 174 BP.
XX
AC AAF27532;
XX
DT 28-MAR-2001 (first entry)
XX
DE Scorpion Bmx1 DNA.
XX
KM Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
XX
KM Hottentotia judaica.
XX
OS WO200078958-A2.
XX
PN 28-DEC-2000.
XX
PD 21-JUN-2000; 2000WO-US017049.
XX
PF 22-JUN-1999; 99US-0140227P.
XX
PR (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Herrmann R, Lee J, Wong JF;
PI
XX
XX WPI; 2001-071394/08.
XX
XX New polynucleotides encoding scorpion venom potassium-channel agonist
PT proteins for production e.g. of insect-tolerant transgenic plants for
PT controlling insect pest damage and parasitic worm infections.
XX
PS Claim 1; Page 48; 50pp; English.
XX
XX The present invention relates to scorpion toxins. The invention may be
CC used for the creation of transgenic plants which express K-channel

CC modifiers, useful as a means for controlling insect pests by producing
 CC insect-tolerant plants. In the prevention and/or treatment of insect pest
 CC damage and parasitic worm infections in animals and humans, the invention
 CC may also find use in creating specific new pesticides and antihelmintic
 CC drugs that are also non-toxic to humans, pets and livestock

XX Sequence 174 BP, 51 A; 25 C; 37 G; 59 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	0.00966	Length:	174
Score:	86.50	Matches:	17
Percent Similarity:	52.27%	Conservative:	6
Best Local Similarity:	38.64%	Mismatches:	20
Query Match:	32.52%	Indels:	1
DB:	4	Gaps:	1

US-10-614-934-14 (1-45) x AAF27532 (1-174)

QY 1 MetMetIlePheCysGlnGlyGlnIleAsnTyraGcCysAsnAsnSerGlyGlu 20
 Db 40 ATAATGATTTCACACCAAGCTCAG---TTTATAGACGTCAATGCAATCACTAAGGAA 96

QY 21 CysIleProHisCysIleArgIleTyraAnthraGalaIaIaIaCysIleAsnIleThr 40
 Db 97 TGTGGCCCTATTGTGAAGAAAGATTGGTGTGCCAAGAGAAAGTGCATTAATAGCAA 156

QY 41 CysAsnCysTyr 44
 Db 157 TGCCCTTCTTAT 168

RESULT 8

ABQ97088 ID ABQ97088 standard; cDNA; 231 BP.

XX AC ABQ97088;

DT 30-OCT-2002 (first entry)

DE Mouse ES cell related cDNA SEQ ID NO 356.

XX Mouse, ES cell; gene trapped sequence; GTS; gene expression;
 KM development disorder; cell differentiation disorder; gene; ss.

XX OS Mus sp.

XX PN US2002081668-A1.

XX PD 27-JUN-2002.

XX PF 30-NOV-2000; 2000US-00728446.

XX PR 20-NOV-1998; 98US-0109302P.

XX PR 01-DEC-1999; 99US-0168270P.

XX PA (FRIE// FRIEDRICH G.

XX PA (ZAMB// ZAMBROWICZ B.

XX PA (SAND// SANDS A T.

XX PA Friedrich G, Zambrowicz B, Sands AT;

XX DR WPI; 2002-626541/67.

XX PT Novel murine polynucleotides that individually identify novel genes into

XX PT which a retroviral gene trap vector has been integrated, useful in

XX PT genomic analysis and in discovery, development of therapeutic and

XX PT diagnostic agents.

XX PS Claim 2; SEQ ID NO 356; 29pp + Sequence Listing; English.

XX CC The invention relates to isolated murine polynucleotides (I) comprising a

XX CC contiguous stretch of at least about 60 nucleotides of a sequence

XX CC (ABQ96733-ABQ98191) chosen from 1461 OMNIBANK gene trapped sequences

XX CC (GTSs). The novel genes can be used in a process to identify novel

CC polynucleotide sequences by comparing them to the novel gene sequences.
 CC The novel genes and cells are useful in functional genomic analysis and
 CC in the discovery and development of new therapeutic and diagnostic agents
 CC and methods. (I) is useful for identifying the coding regions of the
 CC murine genome, to isolate cDNAs, genomic clones or full-length
 CC genes/polynucleotides or homologues, heterologues, paralogues or
 CC orthologues that are capable of hybridizing to one or more of the GTSs
 CC under stringent conditions. (I) can be incorporated into a phage display
 CC system that can be used to screen for proteins or other ligands, that are
 CC capable of binding an amino acid sequence encoded by an oligonucleotide
 CC or polynucleotide sequence in at least one of the GTS sequences. (I) is
 CC useful in arrays, such as gene chips, to identify and characterize
 CC temporal and tissue specific gene expression, to identify the gene of
 CC interest from many sources and for genetic manipulations such as
 CC antisense inhibition and gene targeting. Decreasing the level of
 CC expression of (I) and/or down regulating the activity of peptides or
 CC proteins encoded by (I) is useful for treating development and cell
 CC differentiation disorders. Note: the sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20020081668

XX SQ Sequence 231 BP, 73 A; 47 C; 34 G; 77 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.119	Length:	231
Score:	79.50 <td>Matches:</td> <td>16 </td>	Matches:	16
Percent Similarity:	47.73% <td>Conservative:</td> <td>5 </td>	Conservative:	5
Best Local Similarity:	36.36% <td>Mismatches:</td> <td>20 </td>	Mismatches:	20
Query Match:	29.89% <td>Indels:</td> <td>3 </td>	Indels:	3
DB:	6 <td>Gaps:</td> <td>1 </td>	Gaps:	1

US-10-614-934-14 (1-45) x ABQ97088 (1-231)

QY 4 PheCysGlnGlyGlnIleAsnTyraGcCysAsnAsnSer-----GlyGlu 20

Db 84 TTTCTCTCCAGACAGAAAGCCCTTCTGTAATGTAATCATCAAAAATTTGGCCTC 143

QY 21 CysIleProHisCysIleArgIleTyraAnthraGalaIaIaIaCysIleAsnIleThr 40

Db 144 TGTTCCTCCATTTTGTGGAGATATATCCCATCTTCTAATTCGCACTAGTAAT 203

QY 41 CysAsnCysTyr 44

Db 204 TGTATTCCTT 215

RESULT 9

AAA48437 ID AAA48437 standard; cDNA; 180 BP.

XX AC AAA48437;

DT 15-SEP-2000 (first entry)

DE Scorpion potassium channel agonist Charybdotoxin 2 cDNA.

XX Scorpion, charybdotoxin 2; potassium channel agonist; insecticidal;

KM insect-tolerant transgenic plant; ss.

XX OS Leturus quinquestratus.

XX OS Leturus quinquestratus.

XX OS Leturus quinquestratus.

XX OS Leturus quinquestratus.

XX OS Leturus quinquestratus.

XX OS Leturus quinquestratus.

XX OS Leturus quinquestratus.

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XX OS Leturus quinquestratus.

XX OS Leturus quinquestratus.

XX OS Leturus quinquestratus.

XX OS Leturus quinquestratus.

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XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Herrman R, Wong JF, Lu AL, Presnall JK, Lee J;
XX WPI; 2000-422976/36.
XX P-PSDB; AAY99580.
XX
XX New nucleic acid fragment encoding a scorpion toxin that is a potassium
XX channel agonist, useful for creating transgenic plants that are more
XX insect-tolerant.
XX
XX Claim 2; Page 42; 44pp; English.
XX
XX The present sequence encodes the scorpion potassium channel agonist
XX Charybdotoxin 2. The toxin forms a compact structure kept rigid by three
XX disulphide bonds. Potassium channels modulate a number of cellular events
XX such as muscle contraction, neuro-endocrine secretion, frequency and
XX duration of action potentials, electrolyte homeostasis and resting and
XX membrane potential. The agonist has a high affinity for the channel and
XX may therefore act by producing an irreversible blockade of the channel.
XX The nucleotide sequence was isolated from clone 1st.pK0018-e11 of a cDNA
XX library representing mRNAs from Leiurus scorpion telson tissues. The toxin
XX is insecticidal and the cDNA sequence can therefore be used to create
XX transgenic plants that express the toxin as a means of insect pest
XX control. The amino acid sequence of the present toxin shows homology to
XX the sequence of charybdotoxin 2 from Leiurus quinquestratus (AAY99588)
XX
XX Sequence 180 BP; 57 A; 29 C; 33 G; 61 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.138 Length: 180
XX Score: 78.00 Matches: 13
XX Percent Similarity: 56.67% Conservative: 4
XX Best Local Similarity: 43.33% Mismatches: 13
XX Query Match: 29.32% Indels: 0
XX Gaps: 0
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XX QY 15 CysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsnThrArgAlaAla 34
XX Db 85 TGCAGTGCATCTGCATCATGTGGTGGTTCCTCAAACTGTATAAACACCTCAATGCA 144
XX
XX QY 35 LysCysIleAsnLysThrCysAsnCysTyr 44
XX Db 145 AAGTGTATGAATATATAATGCGCGCTGTAT 174
XX
XX RESULT 10
XX AAA48435
XX ID AAA48435 standard; cDNA; 150 BP.
XX
XX AC AAA48435;
XX
XX DT 15-SEP-2000 (first entry)
XX
XX DE Scorpion potassium channel agonist Charybdotoxin cDNA.
XX
XX KM Scorpion; charybdotoxin; potassium channel agonist; insecticidal;
XX insect-tolerant transgenic plant; ss.
XX
XX OS Leiurus quinquestratus.
XX
XX Key Location/Qualifiers
XX FH 1..150
XX CDS /*tag= a
XX FT /partial
XX FT /product= "Charybdotoxin"
XX
XX WO200032777-A2.
XX
XX 08-JUN-2000.
XX

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PF 01-DEC-1999; 99WO-US028351.
XX
XX 02-DEC-1998; 98US-0110590P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Herrman R, Wong JF, Lu AL, Presnall JK, Lee J;
XX WPI; 2000-422976/36.
XX P-PSDB; AAY99578.
XX
XX New nucleic acid fragment encoding a scorpion toxin that is a potassium
XX channel agonist, useful for creating transgenic plants that are more
XX insect-tolerant.
XX
XX Claim 2; Page 41; 44pp; English.
XX
XX The present sequence encodes the scorpion potassium channel agonist
XX Charybdotoxin. The toxin forms a compact structure kept rigid by three
XX disulphide bonds. Potassium channels modulate a number of cellular events
XX such as muscle contraction, neuro-endocrine secretion, frequency and
XX duration of action potentials, electrolyte homeostasis and resting and
XX membrane potential. The agonist has a high affinity for the channel and
XX may therefore act by producing an irreversible blockade of the channel.
XX The nucleotide sequence was isolated from clone 1st.pK0011.d2 of a cDNA
XX library representing mRNAs from Leiurus scorpion telson tissues. The toxin
XX is insecticidal and the cDNA sequence can therefore be used to create
XX transgenic plants that express the toxin as a means of insect pest
XX control. The amino acid sequence of the present toxin shows homology to
XX the sequence of charybdotoxin from Leiurus quinquestratus (AAY99586)
XX
XX Sequence 150 BP; 43 A; 23 C; 37 G; 47 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.148 Length: 150
XX Score: 77.00 Matches: 13
XX Percent Similarity: 50.00% Conservative: 2
XX Best Local Similarity: 43.33% Mismatches: 15
XX Query Match: 28.95% Indels: 0
XX Gaps: 0
XX
XX US-10-614-934-14 (1-45) x AAA48435 (1-150)
XX
XX QY 15 CysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsnThrArgAlaAla 34
XX Db 58 TGTACTACATCTAAAGATGTGGTGGTTCGAGACATGTATTAAGACCAAGAGGA 117
XX
XX QY 35 LysCysIleAsnLysThrCysAsnCysTyr 44
XX Db 118 AAGTGTATGAATATATAATGCGCGCTGTAT 147
XX
XX RESULT 11
XX AAF27530
XX ID AAF27530 standard; DNA; 176 BP.
XX
XX AC AAF27530;
XX
XX DT 28-MAR-2001 (first entry)
XX
XX DE Scorpion potassium channel blocking toxin 15-1 DNA.
XX
XX KM Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
XX
XX OS Hottentotta judaica.
XX
XX Key Location/Qualifiers
XX FH 1..150
XX CDS /*tag= a
XX FT /partial
XX FT /product= "Charybdotoxin"
XX
XX WO2000078958-A2.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-US017049.
XX
XX 22-JUN-1999; 99US-0140227P.
XX

```

PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Herrmann R, Lee J, Wong JF;
 XX WPI, 2001-071394/08.
 DR New polynucleotides encoding scorpion venom potassium-channel agonist
 PT proteins for production e.g. of insect-tolerant transgenic plants for
 PT controlling insect pest damage and parasitic worm infections.
 XX
 PS Claim 1; Page 47; 50pp; English.
 CC The present invention relates to scorpion toxins. The invention may be
 CC used for the creation of transgenic plants which express K-channel
 CC modifiers, useful as a means for controlling insect pests by producing
 CC insect-tolerant plants. In the prevention and/or treatment of insect pest
 CC damage and parasitic worm infections in animals and humans, the invention
 CC may also find use in creating specific new pesticides and antihelmintic
 CC drugs that are also non-toxic to humans, pets and livestock
 XX
 SQ Sequence 176 BP; 51 A; 24 C; 44 G; 57 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.336 Length: 176
 Score: 75.00 Matches: 13
 Percent Similarity: 52.94% Conservative: 5
 Best Local Similarity: 38.24% Mismatches: 16
 Query Match: 28.20% Indels: 0
 DB: Gaps: 0
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 QY 11 IleaNTYrRGcYsAsnAsnSerGluCysIleProHisCysIleArgIleTyraSn 30
 Db 73 ATAGACGTAAAGTAGTGGCTCTCTGTAATTTGGAGAGCTTGAGAAAAGTAACAGGA 132
 QY 31 ThrARgAlaAlaAlaYsCysIleAsnLysThrCysAsnCySTyr 44
 Db 133 TCAGGACAAAGGAAGTGCAGAAATTAACCAATCTCGTTGTAT 174
 RESULT 12
 AAA48430
 ID AAA48430 standard; cDNA; 177 BP.
 XX
 AC AAA48430;
 XX
 DT 15-SEP-2000 (first entry)
 XX
 DE Scorpion potassium channel blocking toxin 15-1 cDNA.
 XX
 KW Scorpion; potassium channel agonist; insecticidal;
 KW insect-tolerant transgenic plant; potassium channel blocking toxin 15-1;
 XX 88.
 XX Leiurus quinquestriatus.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..177
 FT /*tag= a
 FT /product= "Potassium channel blocking toxin 15-1"
 XX
 FN WO200032777-A2.
 XX
 PD 08-JUN-2000.
 XX
 PE 01-DEC-1999; 99WO-US028351.
 XX
 PR 02-DEC-1998; 98US-0110590P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Herrmann R, Wong JF, Lu AL, Preenail JK, Lee J;
 XX

DR WPI, 2000-422976/36.
 DR P-PSDB; AAY99573.
 XX
 XX New nucleic acid fragment encoding a scorpion toxin that is a potassium
 PT channel agonist, useful for creating transgenic plants that are more
 PT insect-tolerant.
 XX
 PS Claim 2; Page 39; 44pp; English.
 CC The present sequence encodes the scorpion potassium channel blocking
 CC toxin 15-1. The toxin is a potassium channel agonist which forms a
 CC compact structure kept rigid by three disulphide bonds. Potassium
 CC channels modulate a number of cellular events such as muscle contraction,
 CC neuro-endocrine secretion, frequency and duration of action potentials,
 CC electrolyte homeostasis and resting membrane potential. The agonist has a
 CC high affinity for the channel and may therefore act by producing an
 CC irreversible blockade of the channel. The nucleotide sequence was
 CC isolated from clone 18c.pK0005.c5 of a cDNA library representing mRNAs
 CC from Leiurus scorpion telson tissues. The toxin is insecticidal and the
 CC cDNA sequence can therefore be used to create transgenic plants that
 CC express the toxin as a means of insect pest control. The amino acid
 CC sequence of the present toxin shows homology to the sequence of potassium
 CC channel blocking toxin 15-1 from Leiurus quinquestriatus (AAY99581)
 XX
 SQ Sequence 177 BP; 56 A; 25 C; 39 G; 57 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.626 Length: 177
 Score: 73.00 Matches: 14
 Percent Similarity: 45.00% Conservative: 4
 Best Local Similarity: 35.00% Mismatches: 22
 Query Match: 27.44% Indels: 0
 DB: Gaps: 0
 US-10-614-934-14 (1-45) x AAA48430 (1-177)
 QY 5 CysGInGlyGlnLysIleAsnTyraRGcYsAsnAsnSerGluCysIleProHis 24
 Db 55 TGTAGTGAAGCTGCACTATAGAGCTAATGTTTGGATCTCGGAATGTTGGAGAGCT 114
 QY 25 CysIleArgIleTyraSnThrARgAlaAlaAlaYsCysIleAsnLysThrCysAsnCySTyr 44
 Db 115 TGCAGAAAAGTAACAGATCGGACAAAGAAAATGCCAGAAATATCAATGTCGCTGTAT 174
 RESULT 13
 AAF27531
 ID AAF27531 standard; DNA; 177 BP.
 XX
 AC AAF27531;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Scorpion potassium channel blocking toxin 15-1 DNA #2.
 XX
 KW Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
 KW Hottentotta judaica.
 OS
 XX
 FH WO200078958-A2.
 FN 28-DEC-2000.
 PD 21-JUN-2000; 2000WO-US017049.
 XX
 PE 22-JUN-1999; 99US-0140227P.
 XX
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Herrmann R, Lee J, Wong JF;
 XX WPI, 2001-071394/08.
 DR New polynucleotides encoding scorpion venom potassium-channel agonist
 PT

PT proteins for production e.g. of insect-tolerant transgenic plants for
 PT controlling insect pest damage and parasitic worm infections.
 XX
 PS Claim 1; Page 47; 50pp; English.
 XX
 CC The present invention relates to scorpion toxins. The invention may be
 CC used for the creation of transgenic plants which express K-channel
 CC modifiers, useful as a means for controlling insect pests by producing
 CC insect-tolerant plants. In the prevention and/or treatment of insect pest
 CC damage and parasitic worm infections in animals and humans, the invention
 CC may also find use in creating specific new pesticides and antihelminthic
 CC drugs that are also non-toxic to humans, pets and livestock
 XX
 SQ Sequence 177 BP, 61 A, 22 C, 31 G, 63 T, 0 U, 0 Other;
 Alignment Scores:
 Pred. No.: 1.16 Length: 177
 Score: 71.00 Matches: 13
 Percent Similarity: 52.94% Conservative: 5
 Best Local Similarity: 38.24% Mismatches: 16
 Query Match: 26.69% Indels: 0
 DB: Gaps: 0
 US-10-614-934-14 (1-45) x AAF27531 (1-177)
 QY 11 ILeAsnTyArGyCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsn 30
 Db 73 ATAGACGTAATAAGTTTGCATCTCAAGAAATGTTGATTGTTAAAGTAACAGGA 132
 QY 31 ThrArgAlaAlaIysCysIleAsnIysThrCysAsnCysTyr 44
 Db 133 CGGTTTCAGGAAATGCCAGATTAACATGTCGCTGTAT 174
 RESULT 14
 ADR13786
 ID ADR13786 standard; DNA; 435 BP.
 XX
 AC ADR13786;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Chinese scorpion martenotoxin peptide coding sequence.
 XX
 KW Chinese scorpion; martenotoxin; potassium channel blocker; ds; gene.
 XX
 OS Mesobuthus martenensi.
 XX
 PN CN1344745-A.
 XX
 PD 17-APR-2002.
 XX
 PF 12-OCT-2001; 2001CN-00131909.
 XX
 PR 12-OCT-2001; 2001CN-00131909.
 XX
 PA (UIYV) JI Y.
 XX
 PI Ji Y, Li Y, Ye J;
 XX
 DR WPI: 2002-509500/55
 XX
 DR P-PSDB; ADR13780, ADR13781, ADR13790.
 XX
 PT Martenotoxin as one great-conductance calcium-activating potassium channel
 PT blocker and its preparation.
 XX
 PS Disclosure; SEQ ID NO 7; 30pp; Chinese.
 XX
 CC The invention comprises the amino acid and coding sequence of a Chinese
 CC scorpion martenotoxin peptide. The martenotoxin peptide of the invention is
 CC useful as a potassium channel blocker. The present DNA sequence encodes
 CC the Chinese scorpion martenotoxin peptide of the invention.
 XX
 SQ Sequence 435 BP, 148 A, 51 C, 67 G, 169 T, 0 U, 0 Other;

Alignment Scores:
 Pred. No.: 4.93 Length: 435
 Score: 70.00 Matches: 12
 Percent Similarity: 50.00% Conservative: 5
 Best Local Similarity: 35.29% Mismatches: 17
 Query Match: 26.32% Indels: 0
 DB: Gaps: 0
 US-10-614-934-14 (1-45) x ADR13786 (1-435)
 QY 11 ILeAsnTyArGyCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsn 30
 Db 298 ATAGACGTAATAAGTTTGCATCTCAAGAAATGTTGATTGTTAAAGTAACAGGA 357
 QY 31 ThrArgAlaAlaIysCysIleAsnIysThrCysAsnCysTyr 44
 Db 358 TCGGACACAGGAAAGTCCAGAAATCAATCATGTCGATGAC 399
 RESULT 15
 ABN60476/C
 ID ABN60476 standard; cDNA; 598 BP.
 XX
 AC ABN60476;
 XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Human cancer related polynucleotide SEQ ID NO 443.
 XX
 KW Human; cytostatic; gene expression; gene mapping; tissue profiling;
 KW gene therapy; cancer; tumour; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200214500-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 16-AUG-2001; 2001WO-US025840.
 XX
 PR 16-AUG-2000; 2000US-0226326P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 PI Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F,
 PI Lamson G, Scott EM, Zhang G, Kassam A, Pot D, Labat I;
 XX
 DR WPI: 2002-241905/29.
 XX
 PT New nucleic acid for producing a polypeptide, detecting differentially
 PT expressed genes correlated with a cancerous state of a mammalian cell,
 PT and inhibiting tumor growth.
 XX
 PS Claim 1; SEQ ID NO 443; 883pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (ABN27253-ABN33262)
 CC with cytostatic activity. The polynucleotide is used to produce a
 CC polypeptide, to detect differentially expressed genes correlated with a
 CC cancerous state of a mammalian cell and to inhibit tumour growth. The
 CC polynucleotide is used as a probe in mapping and tissue profiling. The
 CC encoded polypeptide and antibodies to the polypeptide can also be used
 CC for therapeutic and diagnostic purposes. The polynucleotide is useful for
 CC gene therapy. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 598 BP, 232 A, 111 C, 134 G, 121 T, 0 U, 0 Other;
 Alignment Scores:
 Pred. No.: 7.38 Length: 598
 Score: 70.00 Matches: 17
 Percent Similarity: 50.98% Conservative: 9

Best Local Similarity: 33.33% Mismatches: 13
 Query Match: 26.32% Indels: 12
 DB: 6 Gaps: 4

US-10-614-934-14 (1-45) x ABN60476 (1-598)

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QY      5  CysGInGIyGInLysLysIle---AsnTYrArGysAsnAsnSerGIyGInCysIlePro 23
          |||::|||
          168 TGTCTGGGCTTTCAAGAGCTGGGATTTACAGGTGTGAGCCCTG-----TGTCTGGAC 115
          |||::|||

QY      24  HisCysIleArGIleTYrAsnThrArGAlaIaIaLysCys-----IleAsn 38
          |||::|||
          114 TACTGCACGTTTCTTACAGCTACTAGTTTAAATGCAACCACTTCATGTAATAATATCA 55
          |||::|||

QY      39  LysThrCys-----AsnCysTYrPro 45
          |||::|||
          54 GAGACTTGCAAAAGTCTAATTCTGTATCTCT 22
          |||::|||
    
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Search completed: August 19, 2005, 05:11:53
 Job time : 436 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2005, 04:24:18 ; Search time 3109 seconds

(without alignments)
550.946 Million cell updates/sec

Title: US-10-614-934-14

Perfect score: 266

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Ygapop 10.0 , Ygapext 0.5	
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_esc2:*
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8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	79.5	29.9	526	BQ033213	UI-1-CFO-AG506152 Mus muscu
C 2	79.5	29.9	766	BQ033213	UI-1-CFO-AG506152 Mus muscu
C 3	79.5	29.9	840	CR177814	Forward s
C 4	79.5	29.9	850	BX977811	Forward s
C 5	79.5	29.9	865	CR245225	Forward s
C 6	79.5	29.9	874	CR257546	Forward s
C 7	79.5	29.9	874	CR173729	EST763049
C 8	73	27.4	794	AG586472	Mus muscu
C 9	72	27.1	187	CV087408	est_c_vir

C 10	72	27.1	345	7	CV087152	est_c_vir
C 11	72	27.1	345	7	CV087280	est_c_vir
C 12	72	27.1	345	7	CV087696	est_c_vir
C 13	72	27.1	345	7	CV087806	est_c_vir
C 14	72	27.1	623	6	CB018045	pgn1c.pk0
C 15	72	27.1	967	4	BG420272	6032448285
C 16	71.5	26.9	605	6	CB280757	
C 17	71.5	26.9	870	9	CC697521	OSVET85TC
C 18	71.5	26.9	932	8	B2966071	PUDFG58TD
C 19	71.5	26.9	932	8	CC389822	PUMMT74TD
C 20	71.5	26.9	964	9	CC697530	OGVET95TM
C 21	70.5	26.5	335	4	BM282738	k139h06.y
C 22	70	26.3	333	2	BB254078	BB254078
C 23	70	26.3	562	9	BX238124	Danilo rer
C 24	69.5	26.1	269	2	BB438608	BB438608
C 25	69.5	26.1	742	9	AG023370	Oryza sat
C 26	69.5	26.1	793	8	AZ135495	OSJNB011
C 27	69.5	26.1	810	7	CK129706	AGENCOURT
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C 31	68.5	25.8	844	8	AZ540533	ENTES79TR
C 32	68.5	25.8	861	8	AZ544428	ENTGP45TF
C 33	68.5	25.8	882	8	AZ668455	ENTMC78TR
C 34	68.5	25.8	899	8	AZ670025	ENTMB20TR
C 35	68.5	25.8	902	8	BZ697287	PUBNB94TD
C 36	68.5	25.8	902	8	AZ540783	ENTDG03TR
C 37	68.5	25.8	910	8	BH135823	ENTQO20TR
C 38	68.5	25.8	940	8	BZ699102	PUMM294TD
C 39	68.5	25.8	960	8	BZ700560	PUBNA94TD
C 40	68.5	25.8	1163	8	CC295363	CH261-64A
C 41	68	25.6	211	1	AV278106	AV278106
C 42	68	25.6	368	8	AQ139514	HS 3088.A
C 43	68	25.6	397	9	CR191328	Forward s
C 44	68	25.6	577	9	CE567579	tigr-gss-
C 45	68	25.6	690	5	B0324729	603489543

ALIGNMENTS

RESULT 1
LOCUS BQ033213/c
DEFINITION UI-1-CFO-axp-g-12-0-UI.s1 NCI CGAP P17r1 Mus musculus cDNA clone.
VERSION BQ033213.1 GI:19768492
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 526)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Minoru Ko, Dr. Janet Rossent, Dr. Janet Rossent

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA sequence: 1-22, >AT rich#low complexity 33-257,
>MER67B#LTR/MER4-group (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.
location/Qualifiers
1. 526

ORIGIN

Alignment Scores:

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 Score: 79.50 Matches: 16
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 Query Match: 29.89% Indels: 3
 DB: 9 Gaps: 1

US-10-614-934-14 (1-45) x CR177814 (1-840)

QY 4 PheCysGInGlyAlaLysLeuAsnTyArgCysAsnAsnSer-----GlyGlu 20
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QY 21 CysIleProHisCysIleArgIleTyAsnThrArgAlaAlaLysCysIleAsnLysThr 40
 DB 712 TGTTCCTCATTTTGTGTGGGAAGATATATATCCCATCTTCTATATTTGCCAAGTAAT 653

QY 41 CysAsnCysTyr 44
 DB 652 TGTATTTGCTTT 641

RESULT 4

BX977811/c BX977811 850 bp DNA linear GSS 05-JUL-2004
 LOCUS Forward strand read from insert in 5'HPT insertion targeting and
 DEFINITION chromosome engineering clone MHPN33h07, genomic survey sequence.

ACCESSION BX977811.1 GI:49709234
 VERSION GSS; genome survey sequence; MICER.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 850)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN33h07"
 /clone_lib="MHPN"
 Location/Qualifiers

ORIGIN

Alignment Scores:

Pred. No.: 5.3 Length: 850
 Score: 79.50 Matches: 16
 Percent Similarity: 47.73% Conservative: 5
 Best Local Similarity: 36.36% Mismatches: 20
 Query Match: 29.89% Indels: 3
 DB: 9 Gaps: 1

US-10-614-934-14 (1-45) x BX977811 (1-850)

QY 4 PheCysGInGlyAlaLysLeuAsnTyArgCysAsnAsnSer-----GlyGlu 20
 DB 770 TTTCCTCCAGACAGAAAGCCCTTCCTTGAATGTAATCATCAAAAAATTTGGCGTC 711

QY 21 CysIleProHisCysIleArgIleTyAsnThrArgAlaAlaLysCysIleAsnLysThr 40
 DB 710 TGTTCCTCATTTTGTGTGGGAAGATATATATCCCATCTTCTATATTTGCCAAGTAAT 651

QY 41 CysAsnCysTyr 44
 DB 650 TGTATTTGCTTT 639

RESULT 5

CR245225/c CR245225 865 bp DNA linear GSS 06-JUL-2004
 LOCUS Forward strand read from insert in 5'HPT insertion targeting and
 DEFINITION chromosome engineering clone MHPN98f06, genomic survey sequence.

ACCESSION CR245225.1 GI:50024079
 VERSION GSS; genome survey sequence; MICER.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 865)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES
 source 1..865
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN98f06"
 /clone_lib="MHPN"
 Location/Qualifiers

ORIGIN

Alignment Scores:

Pred. No.: 5.41 Length: 865
 Score: 79.50 Matches: 16
 Percent Similarity: 47.73% Conservative: 5
 Best Local Similarity: 36.36% Mismatches: 20
 Query Match: 29.89% Indels: 3
 DB: 9 Gaps: 1

US-10-614-934-14 (1-45) x CR245225 (1-865)

QY 4 PheCysGInGlyAlaLysLeuAsnTyArgCysAsnAsnSer-----GlyGlu 20
 DB 781 TTTCCTCCAGACAGAAAGCCCTTCCTTGAATGTAATCATCAAAAAATTTGGCGTC 722

QY 21 CysIleProHisCysIleArgIleTyAsnThrArgAlaAlaLysCysIleAsnLysThr 40
 DB 721 TGTTCCTCATTTTGTGTGGGAAGATATATATCCCATCTTCTATATTTGCCAAGTAAT 662

QY 41 CysAsnCysTyr 44
 DB 661 TGTATTTGCTTT 650

RESULT 6

CR257546/c CR257546 874 bp DNA linear GSS 06-JUL-2004
 LOCUS Forward strand read from insert in 5'HPT insertion targeting and
 DEFINITION chromosome engineering clone MHPN248m09, genomic survey sequence.

ACCESSION CR257546.1 GI:50036399
 VERSION GSS; genome survey sequence; MICER.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 874)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES
 source 1..874
 /organism="Mus musculus"
 Location/Qualifiers

Qy	1	MeemtillephcGcglmcljglnlysllyslleamwtyrargCyaaabnsenrglygu	20
Db	718	CTGCTGCTGTATTTATTATGAAAGAGAAGT---CACATCACATGTTCATAAAAAAGATCA	662
Qy	21	CyslleProhlaeCyslleArgileTyraanthArgalaalalyeCyslleaenlysthr	40
Db	661	TTGATTTCCCACTGATTT---GTATTTAAACTGTACCTAACGACATGTCTGTAAAGCA	605
Qy	41	CysaenCystr 44	
Db	604	TGTCACTACCTAC 593	
RESULT 9			
LOCUS	CV087408/C	187 bp	mRNA linear EST 26-AUG-2004
DEFINITION	est_c_virginica416 Cv Hemo 4hr Immune Forward SSH Crassostrea		
ACCESSION	CV087408		
VERSION	CV087408.1	GI:51566757	
KEYWORDS	EST.		
SOURCE	Crassostrea virginica (eastern oyster)		
ORGANISM	Crassostrea virginica		
REFERENCE	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;		
AUTHORS	Ostreoida; Ostreidae; Crassostrea.		
TITLE	1 (bases 1 to 187)		
JOURNAL	Jenny,M.J., Marr,G.W., Gross,P.S., Almeida,J.S., Chen,Y.,		
COMMENT	McKillen,D.J., Wu,S. and Chapman,R.W. Crassostrea virginica EST Library at marinenomics.org Unpublished (2004) Contact: Gross PS Department of Biochemistry and Molecular Biology Medical University of South Carolina Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA Tel: 846 792 8503 Fax: 843 792 4850 Email: gross@umusc.edu.		
FEATURES	location/Qualifiers		
source	1..187		
	/organism="Crassostrea virginica"		
	/mol_type="mRNA"		
	/db_xref="taxon:6565"		
	/cell_type="Hemocyte"		
	/clone_lib="Cv Hemo 4hr Immune Forward SSH"		
	/note="Vector: pCR2.1; Site_1: none; Site_2: none"		
ORIGIN			
Alignment Scores:			
Pred. No.:	8,21	Length:	187
Score:	72.00	Matches:	11
Percent Similarity:	55.11%	Conservative:	5
Best Local Similarity:	37.93%	Mismatches:	9
Query Match:	27.07%	Indels:	4
DB:	7	Gaps:	1
US-10-614-934-14 (1-45) x CV087408 (1-187)			
Qy	15	CysaenAenSerglyguCyslleProhlaeCyslleArgileTyraanthArgalaal	34
Db	115	TGCACACACATATGCATTTGTTCCGCCCACTGC-----GACCACATTTCTGA	68
Qy	35	LyseCyslleaenlysthrCysaenCys 43	
Db	67	ACTGTATCAACCAATGCCACTGT 41	
RESULT 10			
LOCUS	CV087152/C	345 bp	mRNA linear EST 26-AUG-2004
DEFINITION	est_c_virginica186 Cv Hemo Cadmium Rev SSH Crassostrea virginica		
ACCESSION	CV087152		
VERSION	CV087152.1	GI:51566501	
KEYWORDS	EST.		
SOURCE	Crassostrea virginica (eastern oyster)		

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ORIGIN
Alignment Scores:
Pred. No.: 17.4 Length: 345
Score: 72.00 Matches: 11
Percent Similarity: 55.17% Conservative: 5
Best Local Similarity: 37.93% Mismatches: 9
Query Match: 27.07% Indels: 4
DB: 7 Gaps: 1

US-10-614-934-14 (1-45) x CV087280 (1-345)

QY 15 CysaasnsersgylgucysileprohisCysileargileTyraantThArgAla1a 34
Db 120 TGCACACACATGCTGATTGTTCCGCCCATCTGC-----GACCCACATTCTGGA 73

QY 35 LysCysilleaenlysthrCysaasCys 43
Db 72 ACTTGATCAACAACCAATGCCACTGT 46

RESULT 12
CV087696 345 bp mRNA linear EST 26-AUG-2004
LOCUS est_c_virginica817 Cv Hepato Cadmium Forward SSH Crassostrea
ACCESSION CV087696
VERSION CV087696.1 GI:51567045
KEYWORDS EST.
SOURCE Crassostrea virginica (eastern oyster)
ORGANISM Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
Ostreoidae; Ostreidae; Crassostrea.
REFERENCE 1 (bases 1 to 345)
AUTHORS Jenny,M.J., Marr,G.W., Gross,P.S., Almeida,J.S., Chen,Y.,
McKillen,D.J., Wu,S. and Chapman,R.W.
TITLE Crassostrea virginica EST Library at marinegenomics.org
JOURNAL Unpublished (2004)
CONTACT Gross PS
DEPARTMENT Department of Biochemistry and Molecular Biology
MEDICAL UNIVERSITY of South Carolina
BOX 250509, 173 Ashley Avenue, Charleston, SC 29425, USA
TEL: 846 792 8503
FAX: 843 792 4850
EMAIL: grossp@musc.edu.
FEATURES
SOURCE 1..345
Location/Qualifiers
/organism="Crassostrea virginica"
/mol_type="mRNA"
/db_xref="taxon:6565"
/cell_type="hepatopancreas"
/clone_lib="Cv Hepato Cadmium Forward SSH"
/note="Vector: pCR2.1; Site_1: none; Site_2: none"

ORIGIN
Alignment Scores:
Pred. No.: 17.4 Length: 345
Score: 72.00 Matches: 11
Percent Similarity: 55.17% Conservative: 5
Best Local Similarity: 37.93% Mismatches: 9
Query Match: 27.07% Indels: 4
DB: 7 Gaps: 1

US-10-614-934-14 (1-45) x CV087696 (1-345)

QY 15 CysaasnsersgylgucysileprohisCysileargileTyraantThArgAla1a 34
Db 226 TGCACACACATGCTGATTGTTCCGCCCATCTGC-----GACCCACATTCTGGA 273

QY 35 LysCysilleaenlysthrCysaasCys 43
Db 274 ACTTGATCAACAACCAATGCCACTGT 300

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RESULT 13
CV087806 345 bp mRNA linear EST 26-AUG-2004
LOCUS est_c_virginica546 Cv Hemo 4hr Immune Reverse SSH Crassostrea
DEFINITION virginica cDNA, mRNA sequence.
ACCESSION CV087806
VERSION CV087806.1 GI:51567155
KEYWORDS EST.
SOURCE Crassostrea virginica (eastern oyster)
ORGANISM Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
Ostreoidae; Ostreidae; Crassostrea.
REFERENCE 1 (bases 1 to 345)
AUTHORS Jenny,M.J., Marr,G.W., Gross,P.S., Almeida,J.S., Chen,Y.,
McKillen,D.J., Wu,S. and Chapman,R.W.
TITLE Crassostrea virginica EST Library at marinegenomics.org
JOURNAL Unpublished (2004)
CONTACT Gross PS
DEPARTMENT Department of Biochemistry and Molecular Biology
MEDICAL UNIVERSITY of South Carolina
BOX 250509, 173 Ashley Avenue, Charleston, SC 29425, USA
TEL: 846 792 8503
FAX: 843 792 4850
EMAIL: grossp@musc.edu.
FEATURES
SOURCE 1..345
Location/Qualifiers
/organism="Crassostrea virginica"
/mol_type="mRNA"
/db_xref="taxon:6565"
/cell_type="Hemocyste"
/clone_lib="Cv Hemo 4hr Immune Reverse SSH"
/note="Vector: pCR2.1; Site_1: none; Site_2: none"

ORIGIN
Alignment Scores:
Pred. No.: 17.4 Length: 345
Score: 72.00 Matches: 11
Percent Similarity: 55.17% Conservative: 5
Best Local Similarity: 37.93% Mismatches: 9
Query Match: 27.07% Indels: 4
DB: 7 Gaps: 1

US-10-614-934-14 (1-45) x CV087806 (1-345)

QY 15 CysaasnsersgylgucysileprohisCysileargileTyraantThArgAla1a 34
Db 120 TGCACACACATGCTGATTGTTCCGCCCATCTGC-----GACCCACATTCTGGA 73

QY 35 LysCysilleaenlysthrCysaasCys 43
Db 72 ACTTGATCAACAACCAATGCCACTGT 46

RESULT 14
CB018045
LOCUS CB018045 623 bp mRNA linear EST 10-JAN-2003
DEFINITION psn1c.pk018.012 Chicken lymphoid cDNA library (psn1c) Gallus gallus
cDNA clone psn1c.pk018.012 5' similar to no significant hits
(psn1c(P) 4), mRNA sequence.
ACCESSION CB018045
VERSION CB018045.1 GI:27592781
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 623)
AUTHORS Morgan,R.W. and Burnside,J.
TITLE Chicken ESTs from lymphoid tissue
JOURNAL Unpublished (2002)
CONTACT: Robin W. Morgan
University of Delaware

```


Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1341
Fax: 302 831-2822
Email: morg@udel.edu, www.chickest.udel.edu.

FEATURES

SOURCE

Location/Qualifiers

1. 623
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pgnic.pk018.012"
/sex="Male and Female"
/tissue_type="thymus, bursa, spleen, PBL, bone marrow"
/lab_host="E.coli EMD10B"
/clone_lib="Chicken lymphoid cDNA library (pgnic)"
/note="Vector: pCMVSPORT 6"

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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Percent Similarity:	46.81%						
Best Local Similarity:	36.17%						
Query Match:	27.07%						
DB:	6						

US-10-614-934-14 (1-45) x CB018045 (1-623)

Qy 11 TleantYrArGcYsAaAaAaSerGlyGlu-----Cys 21
Db 223 ATTGAACCTTATGATGAAGAGGGTCTCTTAATAACAGCAGCCCGGTGGCTT 282
Qy 22 TleProHisCysIleArgIleTyrAsnThrArgAlaIalysCysIleAsnLysThrCys 41
Db 283 ATGCTTCACAGCAGAGAGGTTTATAT-----GCCGAAATGTTTATCTTCATTATGT 336
Qy 42 AaAcys-----TyrPro 45
Db 337 AACTGTGATGTGATTACCA 357

RESULT 15

LOCUS

BG420272/c 967 bp mRNA linear EST 14-MAR-2001

DEFINITION

602448285F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4586972 5', mRNA sequence.

ACCESSION

BG420272

KEYWORDS

BG420272.1 GI:13326778

SOURCE

EST.

ORGANISM

Homo sapiens (human)

REFERENCE

1 (bases 1 to 967)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

FEATURES

Location/Qualifiers

1. 967
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4586972"

FEATURES

SOURCE

Location/Qualifiers

1. 967
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4586972"

/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 14"
/note="Organ: kidney; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
61.6	72.00	967	14	5	8	4	1
Percent Similarity:	61.29%						
Best Local Similarity:	45.16%						
Query Match:	27.07%						
DB:	4						

US-10-614-934-14 (1-45) x BG420272 (1-967)

Qy 3 TlephecYsgInGlyGlnLysIleAsnTyrArGcYsAaAaAaSerGlyGluCysIle 22
Db 780 ATTTTGTATGATGATGAAGAGGTTTATCGATGAGTGCCCACTCGTGAC----- 727
Qy 23 ProHisCysIleArgIleTyrAsnThrArgAla 33
Db 726 -----TGTGTGCGTTTTCATACACAGGGCA 700

Search completed: August 19, 2005, 06:33:27
Job time : 3114 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 10:20:42 ; Search time 131 Seconds

(without alignments)
562.080 Million cell updates/sec

Title: US-10-614-934-14

Perfect score: 266

Sequence: 1 MMIFCQKIKINRCNNGSE.....IRIYNTBAKCNKNCYCYP 45

Scoring table:

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	Ygapop 10.0 , Ygapext 0.5
	Fgapop 6.0 , Fgapext 7.0
	Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QEMT=fastap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10614934@cgn2_1.1.105@rnat_19082005_112037_24047 -NCPU=6 -ICPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSFLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*

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- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	266	100.0	138	4	US-09-857-401B-13
2	101	38.0	114	4	US-09-857-401B-9
3	92.5	34.8	186	4	US-10-044-359-3
4	91.5	34.4	154	1	US-08-096-942-5
5	91.5	34.4	154	1	PCT-US94-08063-5
6	87.5	33.9	180	4	US-10-044-359-5
7	86.5	33.5	120	1	US-08-096-942-2
8	86.5	33.5	174	4	US-10-044-359-19
9	78	23.3	180	4	US-09-857-401B-15
10	77	23.9	150	4	US-09-857-401B-11
11	75	28.2	176	4	US-10-044-359-15
12	73	27.4	177	4	US-09-857-401B-1

13	71	26.7	177	4	US-10-044-359-17
14	68.5	25.8	127	5	PCT-US94-08063-2
15	68.5	25.8	124700	4	US-09-949-016-11817
16	68.5	25.8	124701	4	US-09-949-016-15439
17	67.5	25.4	643	4	US-09-270-767-5432
18	67.5	25.4	643	4	US-09-270-767-20714
19	64	24.1	601	4	US-09-949-016-51773
20	64	24.1	146095	4	US-09-949-016-12872
21	64	24.1	146104	4	US-09-949-016-13239
22	63	23.7	891	4	US-09-810-886B-7
23	63	23.7	2940	3	US-08-688-421-28
24	63	23.7	2940	3	US-09-389-528-28
25	63	23.7	2940	3	US-09-181-8274-28
26	62	23.3	544	4	US-09-621-976-15220
27	62	23.3	636591	4	US-09-949-016-11808
28	62	23.3	636591	4	US-09-949-016-13388
29	61.5	23.1	817	4	US-09-270-767-12401
30	61.5	23.1	2964	2	US-08-286-819A-18
31	61.5	23.1	2964	3	US-08-980-357-18
32	61.5	23.1	3190	2	US-08-286-819A-30
33	61.5	23.1	3190	3	US-08-980-357-30
34	61.5	23.1	7577	3	US-08-961-527-46
35	61.5	23.1	10851	2	US-08-286-819A-16
36	61.5	23.1	10851	3	US-08-980-357-16
37	61	22.9	1167	4	US-09-489-039A-1018
38	60.5	22.7	640	4	US-08-956-171E-418
39	60.5	22.7	640	4	US-08-781-986A-418
40	60.5	22.7	2581	1	US-08-200-900A-1
41	60.5	22.7	2581	4	US-08-794-042-1
42	60.5	22.7	2581	5	PCT-US94-00616-1
43	60.5	22.7	3576	4	US-09-540-236-982
44	60	22.6	349	4	US-09-621-976-15221
45	60	22.6	1128	3	US-08-976-259-25

ALIGNMENTS:

US-09-857-401B-13
Sequence 13, Application US/09857401B
Patent No. 6593141
GENERAL INFORMATION:
APPLICANT: HERRMANN, RAFAEL
APPLICANT: WONG, JAMES F.
APPLICANT: LU, ALBERT L.
APPLICANT: PRESNALL, JAMES K.
APPLICANT: LEE, JIAN-MING
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: B01102
CURRENT APPLICATION NUMBER: US/09/857,401B
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/110,590
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 138
TYPE: DNA
ORGANISM: Leirus quinquestriatus
US-09-857-401B-13

Alignment Scores:
Pred. No.: 3,586-29
Score: 266.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0

US-10-614-934-14 (1-45) x US-09-857-401B-13 (1-138)

QY 1 MetMetIleIlepeCgGInGlyGInLysIleAsnTYrArgCYaAsnAsnSerGlyGlu 20
|||||

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Db 1 ATGATGATTTTCGCCAAGCCGAGAAAAAATAATTATCATGTATATATACGGGTGAG 60
Qy 21 CysileProhiscysileargiletyrAsnthrgalaalysCysileAsnlysthr 40
Db 61 TGTATTCACATTCATCATAGATATATATACACGAGAGCAAGTGTATTAATAAACA 120
Qy 41 CysAsnCysTyPro 45
Db 121 TGCATTTGTTATCA 135

RESULT 2
US-09-857-401B-9
; Sequence 9, Application US/09857401B
; Patent No. 6593141
; GENERAL INFORMATION:
; APPLICANT: HERMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/09/857,401B
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Leirurus quinquestrictus
US-09-857-401B-9

Alignment Scores:
Pred. No.: 4.63e-06 Length: 114
Score: 101.00 Matches: 17
Percent Similarity: 58.82% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 14
Query Match: 37.97% Indels: 0
Gaps: 0

US-10-614-934-14 (1-45) x US-09-857-401B-9 (1-114)
Qy 12 AsnTyrrArgCysAsnAsnSerGlyGluCysileProhiscysileargiletyrAsnthr 31
Db 10 AATGTGCCGTCAGAAATTTCTGACAAATGTCTCCAGTTGCATTAATAAAGTAATAT 69
Qy 32 ArgAlaAlaAlysCysileAsnlysthrCysAsnCysTyPro 45
Db 70 AATAGCGGAAAGTGTGTAAAGACAAAGTATTTGTTATCA 111

RESULT 3
US-10-044-359-3
; Sequence 3, Application US/10044359
; Patent No. 6740743
; GENERAL INFORMATION:
; APPLICANT: Herrman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 186
; TYPE: DNA
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; ORGANISM: Hottentotta judaica
US-10-044-359-3

Alignment Scores:
Pred. No.: 0.000142 Length: 186
Score: 92.50 Matches: 17
Percent Similarity: 50.00% Conservative: 6
Best Local Similarity: 36.96% Mismatches: 22
Query Match: 34.77% Indels: 1
Gaps: 1

US-10-614-934-14 (1-45) x US-10-044-359-3 (1-186)
Qy 1 MetwettllephecysginglyGlnlyslsleAsnTyrrArgCys--AsnAsnSerGly 19
Db 46 ATGTTATTTTCGAGCCAGCTCAATACGAGTTGATGATGATGATGATGATGATGATGAT 105
Qy 20 GluCysileProhiscysileargiletyrAsnthrgalaalysCysileAsnlysthr 39
Db 106 AATTGCGTAAACCACTATGTATTAATACGGCACAACCTAAACTAATGATCAACGAT 165
Qy 40 ThrCysAsnCysTyPro 45
Db 166 CGGTGCAACTGTATTCG 183

RESULT 4
US-08-096-942-5
; Sequence 5, Application US/08096942
; Patent No. 5494895
; GENERAL INFORMATION:
; APPLICANT: GARCIA, MARIA L
; APPLICANT: KOO, GLORIA C
; APPLICANT: LEONARD, REID J
; APPLICANT: LIN, CHIU-CHUAN S
; APPLICANT: SLAUGHTER, ROBERT S
; APPLICANT: STEVENS, SCOTT P
; APPLICANT: WILLIAMSON, JOANNE M
; TITLE OF INVENTION: SCORPION PEPTIDE WITH IMMUNOSUPPRESSANT
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CATHERINE A. DOLAN, MERCK & CO., INC.
; STREET: P.O. BOX 2000, 126 LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,942
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DOLAN, CATHERINE A
; REGISTRATION NUMBER: 36502
; REFERENCE/DOCKET NUMBER: 18952
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4283
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-096-942-5
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[illegible]

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      PRIOR APPLICATION NUMBER: 60/140,227
      PRIOR FILING DATE: 1999-06-22
      NUMBER OF SEQ ID NOS: 28
      SOFTWARE: Microsoft Office 97
      SEQ ID NO 19
      LENGTH: 174
      TYPE: DNA
      ORGANISM: Hottentotta judaica
      FEATURE:
      NAME/KEY: unsure
      LOCATION: (9)
      FEATURE:
      NAME/KEY: unsure
      LOCATION: (88)
      US-10-044-359-19

Alignment Scores:
Pred. NO.: 0.000905      Length: 174
Score: 86.50      Matches: 17
Percent Similarity: 52.27%      Conservative: 6
Best Local Similarity: 38.64%      Mismatches: 20
Query Match: 32.52%      Indels: 1
DB: 4      Gaps: 1

US-10-614-934-14 (1-45) x US-10-044-359-19 (1-174)

QY      1 MetwEllephecYscngIyGInuLySllEaEnTyraYcYsaSaNsSergIyGIn 20
      ::::::::::::::::::::
DB      40 ATATGATTTCAACCGAAGCTCAG--TTTATGACGTGAATGCACATCACTAAGCA 96
QY      21 CysElleProhIacYsIlleAagIleTyraEnThrArGAlAlAlLyCyCysElleAsnIySthr 40
      |||||
DB      97 TGTGGGCTATTGTTGTAAGGAAAGATTGGTGTGGCCAGAGAAAGTGCATTAATAAGCA 15
QY      41 CysaSnCysTyr 44
      |||||
DB      157 TGCCGTTGTTAT 168

RESULT 9
US-09-857-401B-15
; Sequence 15, Application US/09857401B
; Patent No. 6593141
; GENERAL INFORMATION:
; APPLICANT: HERMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/09/857,401B
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Leiurus quinquestriatus
US-09-857-401B-15

Alignment Scores:
Pred. NO.: 0.0149      Length: 180
Score: 78.00      Matches: 13
Percent Similarity: 56.67%      Conservative: 4
Best Local Similarity: 43.33%      Mismatches: 13
Query Match: 29.32%      Indels: 0
DB: 4      Gaps: 0

US-10-614-934-14 (1-45) x US-09-857-401B-15 (1-180)

15 CysaSaNsSergIyGInuLyCysIlleProhIacYsIlleAagIleTyraEnThrArGAlAlAla 34

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; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Hottentotta judaica
US-10-044-359-17

Alignment Scores:
Pred. No.: 0.141 Length: 177
Score: 71.00 Matches: 13
Percent Similarity: 52.94% Conservative: 5
Best Local Similarity: 38.24% Mismatches: 16
Query Match: 26.69% Indels: 0
DB: 4 Gaps: 0

US-10-614-934-14 (1-45) x US-10-044-359-17 (1-177)
Qy 11 leasntYrargCysAsnaSenSerGlyGluCysileProHisCysileArgileTyraSn 30
Db 73 ATGACGCTAAATATATTCTTCATCTCAAGAAATGTTGATGCTGTGTAATAAAGTAACCTGGA 132
Qy 31 ThrArgAlaAlaLysCysileAsnLysThrCysAsnCysTyR 44
Db 133 CGGTTTCAGGAAGAAATGCCAAGATTAACAATGTCGCTGTAT 174

RESULT 14
PCT-US94-08063-2
; Sequence 2, Application PC/TUS9408063
; GENERAL INFORMATION:
; APPLICANT: GARCIA, MARIA L
; APPLICANT: KOO, GLORIA C
; APPLICANT: LEONARD, REID J
; APPLICANT: LIN, CHU-CHUAN S
; APPLICANT: SLAUGHTER, ROBERT S
; APPLICANT: STEVENS, SCOTT P
; APPLICANT: WILLIAMSON, JOANNE M
; TITLE OF INVENTION: SCORPION PEPTIDE WITH IMMUNOSUPPRESSANT
; TITLE OF INVENTION: ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FRANK P. BIGLEY, MERCK & CO., INC.
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08063
; FILING DATE: 22-JUL-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGLEY, FRANK P.
; REGISTRATION NUMBER: 36356
; REFERENCE/DOCKET NUMBER: 18952P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-1249
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US94-08063-2

Alignment Scores:
Pred. No.: 0.201 Length: 127
Score: 68.50 Matches: 15
Percent Similarity: 53.85% Conservative: 6
Best Local Similarity: 38.46% Mismatches: 14
Query Match: 25.75% Indels: 4
DB: 5 Gaps: 1

US-10-614-934-14 (1-45) x PCT-US94-08063-2 (1-127)
Qy 11 leasntYrargCysAsnaSenSerGlyGluCysileProHisCysileArgileTyraSn 30
Db 7 ATGACGCTAAATATGCACTCTCCGAAACAGTCTGCCGCCGTCGCAAGCTCACTTCGCT 66
Qy 31 ThrArgAla-----AlaLysCysileAsnLysThrCysAsnCysTyRPro 45
Db 67 CAGTCTGCTGCTGCTAAATGCTAAATGCAATGAAAGTAATGCAATGTAACCG 121

RESULT 15
US-09-949-016-11817
; Sequence 11817, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11817
; LENGTH: 124700
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11817

Alignment Scores:
Pred. No.: 2.41e+03 Length: 124700
Score: 68.50 Matches: 15
Percent Similarity: 38.98% Conservative: 8
Best Local Similarity: 25.42% Mismatches: 19
Query Match: 25.75% Indels: 17
DB: 4 Gaps: 1

US-10-614-934-14 (1-45) x US-09-949-016-11817 (1-124700)
Qy 4 PhnCysGlnGlyGluLysLysileAsnLysThrCysAsnaSenSerGlyGlu----- 20
Db 91091 TTCTGTGAAATTTCCAGAGTGCGAGATCATCTTAACAGTAACAGAACAGATCATCAT 91150
Qy 21 -----CysileProHisCysile 26
Db 91151 CCTCCATCCAGATTAAACAATGTTTGTATGATATTGCTTTCAGCATTTGTTG 91210
Qy 27 Arg11leTyraSenThrArgAlaAlaLysCysileAsnLysThrCysAsnCysTyRPro 45
Db 91211 TTGACTTATGTAATAACCCACTACAGGTGATCAGTATCTCGCAACTGTATCC 91267

Search completed: August 19, 2005, 10:23:20
Job time : 144 secs

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Fri Aug 19 10:52:13 2005

us-10-614-934-14.rml

Page 7

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GenCore version 5.1.6
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OM protein - nucleic search, using .frame_plus_p2n model

Run on: August 19, 2005, 03:05:35 ; Search time 622 Seconds

(without alignments)
470.034 Million cell updates/sec

Title: US-10-614-934-14

Perfect score: 266

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORES=pc -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USR=US10614934.@cgn_1.1.723.@rnatc_17082005_181355_22021
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	266	100.0	138	21	US-10-614-934-13	Sequence 13, Appl
2	101	38.0	114	21	US-10-614-934-9	Sequence 9, Appl
3	92.5	34.8	186	13	US-10-044-359-3	Sequence 3, Appl
4	87.5	32.9	180	13	US-10-044-359-5	Sequence 5, Appl
5	86.5	32.5	174	13	US-10-044-359-19	Sequence 19, Appl
6	79.5	29.9	231	9	US-09-728-446-356	Sequence 356, App
7	78	29.3	180	21	US-10-614-934-15	Sequence 15, Appl
8	77	28.9	150	21	US-10-614-934-11	Sequence 11, Appl
9	75	28.2	176	13	US-10-044-359-15	Sequence 15, Appl
10	73	27.4	177	21	US-10-614-934-1	Sequence 1, Appl
11	71.5	26.9	905	18	US-10-425-114-17548	Sequence 17548, A
12	71.5	26.9	1405	18	US-10-425-114-23882	Sequence 23882, A
13	71.5	26.9	1770	20	US-10-425-115-38932	Sequence 38932, A
14	71.5	26.9	2525	20	US-10-425-115-38929	Sequence 38929, A
15	71	26.7	177	13	US-10-044-359-17	Sequence 17, Appl
16	69.5	26.1	3846	19	US-10-437-963-33842	Sequence 33842, A
17	68.5	25.8	73100	19	US-10-319-914-11	Sequence 11, Appl
18	68	25.6	350570	20	US-10-417-375-146	Sequence 146, App
19	66.5	25.0	83009	20	US-10-417-375-143	Sequence 143, App
20	66	24.8	204	21	US-10-721-793-131	Sequence 131, App
21	66	24.8	323	21	US-10-721-793-129	Sequence 129, App
22	66	24.8	626	13	US-10-027-632-281127	Sequence 281127, A
23	66	24.8	626	17	US-10-027-632-281127	Sequence 281127, A
24	65.5	24.6	377	20	US-10-425-115-166413	Sequence 166413, A
25	65	24.4	288	19	US-10-437-963-57403	Sequence 57403, A
26	65	24.4	316	19	US-10-437-963-11987	Sequence 11987, A
27	64	24.1	2185	17	US-10-104-047-556	Sequence 556, App
28	64	24.1	2422	19	US-10-437-963-4897	Sequence 4897, App
29	64	24.1	42360	19	US-10-367-094-148	Sequence 148, App
30	64	24.1	143306	9	US-09-729-920-3	Sequence 3, Appl
31	64	24.1	143306	20	US-10-887-932-3	Sequence 3, Appl
32	63.5	23.9	3543	18	US-10-369-493-34016	Sequence 34016, A
33	63.5	23.9	1552	18	US-10-425-114-26499	Sequence 26499, A
34	63.5	23.9	50000	21	US-10-706-635-24	Sequence 24, Appl
35	63.5	23.9	366710	20	US-10-719-993-5792	Sequence 5792, App
36	63	23.7	533	16	US-10-029-386-5501	Sequence 5501, App
37	63	23.7	671	13	US-10-027-632-15307	Sequence 15307, A
38	63	23.7	671	13	US-10-027-632-15307	Sequence 15307, A
39	63	23.7	671	17	US-10-027-632-15307	Sequence 15307, A
40	63	23.7	671	17	US-10-027-632-15308	Sequence 15308, A
41	63	23.7	891	14	US-09-810-836B-7	Sequence 7, Appl
42	63	23.7	891	14	US-10-286-264-53	Sequence 63, Appl
43	63	23.7	891	15	US-10-295-403-21	Sequence 21, Appl
44	63	23.7	891	17	US-10-225-066A-559	Sequence 559, App
45	63	23.7	891	17	US-10-374-780A-2437	Sequence 2437, App

ALIGNMENTS

RESULT 1
US-10-614-934-13
; Sequence 13, Application US/10614934
; Publication No. US20050042717A1
GENERAL INFORMATION:
APPLICANT: HERRMANN, RAFAEL
APPLICANT: WONG, JAMES F.
APPLICANT: LU, ALBERT L.
APPLICANT: PRESNALL, JAMES K.
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: B11102
CURRENT APPLICATION NUMBER: US/10/614,934
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/857,401
PRIOR FILING DATE: 2001-06-01

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; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 138
; TYPE: DNA
; ORGANISM: Leivirus quinquestrictus
US-10-614-934-13

Alignment Scores:
Pred. No.: 1,14e-27 Length: 138
Score: 266.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-13 (1-138)

Qy 1 MetNcIlePheCySGInGlyGlnIylsIleAsnTyRgCYsAsnAsnSerGlyGlu 20
Db 1 ATGATGATTTCTGCGCAAGCCAGAAAATAATTTCATGTAATTAATAGCGGTAG 60

Qy 21 CysIleProHisCySIIeArgIIeTyRAsnThrArgIaIaIySCySIIeAsnIylsThr 40
Db 61 TGTATTCCACATGTCATCAGATATATATTAACACAGACGAGAAAGTGTATTATAAACA 120

Qy 41 CysAsnCYsTYrPro 45
Db 121 TGCATTGTATTCCA 135

RESULT 2
US-10-614-934-9
; Sequence 9, Application US/10614934
; Publication No. US20050042717A1
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/10/614,934
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/857,401
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Leivirus quinquestrictus
US-10-614-934-9

Alignment Scores:
Pred. No.: 5.05e-05 Length: 114
Score: 101.00 Matches: 17
Percent Similarity: 58.82% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 14
Query Match: 37.97% Indels: 0
DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-9 (1-114)

Qy 12 AsnTyRgCYsAsnAsnSerGlyGluCYsIleProHisCySIIeArgIIeTyRAsnThr 31
Db 10 AATGCGCGGTGCAAGAAATTTCTGACATGTCGTCAGTTTCATTAATAAAGTAATAT 69

Qy 32 ArgIaIaIySCySIIeAsnIylsThrCYsAsnCYsTYrPro 45
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Db 70 AATGCGGAAAGTGTGTAATGACCAATGTATTGTATCCA 111

RESULT 3
US-10-044-359-3
; Sequence 3, Application US/10044359
; Publication No. US20020160454A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 186
; TYPE: DNA
; ORGANISM: Hottentotca judaica
US-10-044-359-3

Alignment Scores:
Pred. No.: 0.00141 Length: 186
Score: 92.50 Matches: 17
Percent Similarity: 50.00% Conservative: 6
Best Local Similarity: 36.96% Mismatches: 22
Query Match: 34.77% Indels: 1
DB: 13 Gaps: 1

US-10-614-934-14 (1-45) x US-10-044-359-3 (1-186)

Qy 1 MetNcIlePheCySGInGlyGlnIylsIleAsnTyRgCYs---AsnAsnSerGly 19
Db 46 ATGGTATTTCGAGCCAGCTCAATACGAGTTGATGTAACGTGTATGGAGAGAGAT 105

Qy 20 GlucySIIeProHisCySIIeArgIIeTyRAsnThrArgIaIaIySCySIIeAsnIyls 39
Db 106 AATGCGTAAACCATCTATGATTAATACGGCACAACTAAATGATCAACGAT 165

Qy 40 ThrCYsAsnCYsTYrPro 45
Db 166 CGGTGCACTGTATTCCG 183

RESULT 4
US-10-044-359-5
; Sequence 5, Application US/10044359
; Publication No. US20020160454A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Hottentotca judaica
US-10-044-359-5
```

Alignment Scores:

Pred. No.: 0.0066 Length: 180
 Score: 87.50 Matches: 18
 Percent Similarity: 46.67% Conservative: 3
 Best Local Similarity: 40.00% Mismatches: 23
 Query Match: 32.89% Indels: 1
 DB: 13 Gaps: 1

US-10-614-934-14 (1-45) x US-10-044-359-5 (1-180)

QY 1 MetMetIlePheCysGlnGlyInlySylleAntYrAsgCysAsnAsnSerGlyGlu 20
 Db 46 ATGACCATATGATTAATTCAGAGTAAACAAATGTGAATGT---ACAGGTGCTCA 102
 QY 21 CysIleProHisCysIleArgIleTyraAntHraGAlaAlaIleCysIleAsnlySThr 40
 Db 103 TGTGCTTCAACTGTATTAAGAGTAATGAGTAGTCTGCGAATAATGCTTATATGAGACA 162
 QY 41 CysAsnCysTyrPro 45
 Db 163 TGTGTCTGCTATCCG 177

RESULT 5

US-10-044-359-19
 ; Sequence 19, Application US/10044359
 ; Publication No. US20020160454A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herrman, Rafael
 ; APPLICANT: Wong, James F.
 ; APPLICANT: Lee, Jian-Ming
 ; TITLE OF INVENTION: SCORPION TOXINS
 ; FILE REFERENCE: BB1367 US NA
 ; CURRENT APPLICATION NUMBER: US/10/044,359
 ; PRIOR FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: 09/599,416
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 60/140,227
 ; PRIOR FILING DATE: 1999-06-22
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 19
 ; LENGTH: 174
 ; TYPE: DNA
 ; ORGANISM: Hottentotta judaica
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (9)
 ; NAME/KEY: unsure
 ; LOCATION: (88)
 ; US-10-044-359-19

Alignment Scores:

Pred. No.: 0.00869 Length: 174
 Score: 86.50 Matches: 17
 Percent Similarity: 52.27% Conservative: 6
 Best Local Similarity: 38.64% Mismatches: 20
 Query Match: 32.52% Indels: 1
 DB: 13 Gaps: 1

US-10-614-934-14 (1-45) x US-10-044-359-19 (1-174)

QY 1 MetMetIlePheCysGlnGlyInlySylleAntYrAsgCysAsnAsnSerGlyGlu 20
 Db 40 ATTAATGATTTCAACGAGCTGAG--TTTATGACGTGAATAATGACATCAGCTAAGCA 96
 QY 21 CysIleProHisCysIleArgIleTyraAntHraGAlaAlaIleCysIleAsnlySThr 40
 Db 97 TGTGCGCATTTGTTAAGAGAAATTTGTTGTGGCAGAGAAAGTGCATTAATAAGCA 156
 QY 41 CysAsnCysTyr 44
 Db 157 TGCCTGTGTAT 168

RESULT 6

US-09-728-446-356
 ; Sequence 356, Application US/09728446
 ; Patent No. US20020081668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. US20020081668A1 Murine Polynucleotide Sequences
 ; FILE REFERENCE: LEX-0101-USA
 ; CURRENT APPLICATION NUMBER: US/09/728,446
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/168,270
 ; PRIOR FILING DATE: 1999-12-01
 ; NUMBER OF SEQ ID NOS: 1461
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 356
 ; LENGTH: 231
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; US-09-728-446-356

Alignment Scores:

Pred. No.: 0.115 Length: 231
 Score: 79.50 Matches: 16
 Percent Similarity: 47.73% Conservative: 5
 Best Local Similarity: 36.36% Mismatches: 20
 Query Match: 29.89% Indels: 3
 DB: 9 Gaps: 1

US-10-614-934-14 (1-45) x US-09-728-446-356 (1-231)

QY 4 PheCysGlnGlyInlySylleAntYrAsgCysAsnAsnSer-----GlyGlu 20
 Db 84 TTTCTCCAGGACAGAAAGCCCTTCTTGAATGTAAATCTCAAAAATTTTGCCGTC 143
 QY 21 CysIleProHisCysIleArgIleTyraAntHraGAlaAlaIleCysIleAsnlySThr 40
 Db 144 TGTTCCTCATTTTGTGTGGAGATATATATCCATCTTCTATTAATTCAGTAAAT 203
 QY 41 CysAsnCysTyr 44
 Db 204 TGTATTCCTT 215

RESULT 7

US-10-614-934-15
 ; Sequence 15, Application US/10614934
 ; Publication No. US20050042717A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HERRMANN, RAFAEL
 ; APPLICANT: WONG, JAMES F.
 ; APPLICANT: LU, ALBERT L.
 ; APPLICANT: PRESNAIL, JAMES K.
 ; APPLICANT: LEE, JIAN-MING
 ; TITLE OF INVENTION: SCORPION TOXINS
 ; FILE REFERENCE: BB1102
 ; CURRENT APPLICATION NUMBER: US/10/614,934
 ; PRIOR FILING DATE: 2003-07-08
 ; PRIOR APPLICATION NUMBER: US/09/857,401
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: 60/110,590
 ; PRIOR FILING DATE: 1998-12-02
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 15
 ; LENGTH: 180
 ; TYPE: DNA
 ; ORGANISM: Leiurus quinquestriatus
 ; US-10-614-934-15

Alignment Scores:

Pred. No.: 0.135 Length: 180
 Score: 78.00 Matches: 13
 Percent Similarity: 56.67% Conservative: 4
 Best Local Similarity: 43.33% Mismatches: 13
 Query Match: 29.32% Indels: 0
 DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-15 (1-180)

QY 15 CysaanaenSerglyGluCysIleProHisCysIleArgIleTyraSntHrArgAlaAla 34
 Db 85 TGCAGTGCATCTGCATCATCTGTTGGTTGTTCTCAAACTGTATTAACACCTCATGCA 144

QY 35 LysCysIleAenlySthrCysaSnCysTyr 44
 Db 145 AAGTGTATGATTAATTAATGCCGCTGTAT 174

RESULT 8
 US-10-614-934-11

; Sequence 11, Application US/10614934
 ; Publication No. US20050042717A1
 ; GENERAL INFORMATION:

; APPLICANT: HERMANN, RAFAEL
 ; APPLICANT: WONG, JAMES F.
 ; APPLICANT: LU, ALBERT L.
 ; APPLICANT: PRESNAIL, JAMES K.
 ; APPLICANT: LEE, JIAN-MING
 ; TITLE OF INVENTION: SCORPION TOXINS
 ; FILE REFERENCE: BB1102
 ; CURRENT APPLICATION NUMBER: US/10/614,934
 ; CURRENT FILING DATE: 2003-07-08
 ; PRIOR APPLICATION NUMBER: US/09/857,401
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: 60/110,590
 ; PRIOR FILING DATE: 1998-12-02
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 11
 ; LENGTH: 150
 ; TYPE: DNA
 ; ORGANISM: Leiurus quinquestriatus
 US-10-614-934-11

Alignment Scores:
 Pred. No.: 0.146 Length: 150
 Score: 77.00 Matches: 13
 Percent Similarity: 50.00% Conservative: 2
 Best Local Similarity: 43.33% Mismatches: 15
 Query Match: 28.95% Indels: 0
 DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-11 (1-150)

QY 15 CysaanaenSerglyGluCysIleProHisCysIleArgIleTyraSntHrArgAlaAla 34
 Db 58 TGTACTACATCTAAAGAAATGTTGGTGTGTGAGACATTGTATTAAGACCAAGAGAGA 117

QY 35 LysCysIleAenlySthrCysaSnCysTyr 44
 Db 118 AAGTGCATGATTTGGAATGCCGCTGTAT 147

RESULT 9
 US-10-044-359-15

; Sequence 15, Application US/10044359
 ; Publication No. US20020160454A1
 ; GENERAL INFORMATION:

; APPLICANT: Herrman, Rafael
 ; APPLICANT: Wong, James F.
 ; APPLICANT: Lee, Jian-Ming
 ; TITLE OF INVENTION: SCORPION TOXINS
 ; FILE REFERENCE: BB1367 US NA
 ; CURRENT APPLICATION NUMBER: US/10/044,359
 ; CURRENT FILING DATE: 2002-01-11

; PRIOR APPLICATION NUMBER: 09/599,416
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 60/140,227
 ; PRIOR FILING DATE: 1999-06-22
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 15
 ; LENGTH: 176
 ; TYPE: DNA
 ; ORGANISM: Hottentotta judaica
 US-10-044-359-15

QY 11 IleaSntYrArgCysaanaenSerglyGluCysIleProHisCysIleArgIleTyraSn 30
 Db 73 ATGACGTAAAGATGATGCTCTCGTGAATGTGGAGAGCTTCAGAAAAGTAACAGCA 132

QY 31 ThrArgAlaAlaLysCysIleAenlySthrCysaSnCysTyr 44
 Db 133 TCAGACAGAGAAAGTCCAGAAATTAACCAATGTCGTGTAT 174

RESULT 10
 US-10-614-934-1

; Sequence 1, Application US/10614934
 ; Publication No. US20050042717A1
 ; GENERAL INFORMATION:

; APPLICANT: HERMANN, RAFAEL
 ; APPLICANT: WONG, JAMES F.
 ; APPLICANT: LU, ALBERT L.
 ; APPLICANT: PRESNAIL, JAMES K.
 ; APPLICANT: LEE, JIAN-MING
 ; TITLE OF INVENTION: SCORPION TOXINS
 ; FILE REFERENCE: BB1102
 ; CURRENT APPLICATION NUMBER: US/10/614,934
 ; CURRENT FILING DATE: 2003-07-08
 ; PRIOR APPLICATION NUMBER: US/09/857,401
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: 60/110,590
 ; PRIOR FILING DATE: 1998-12-02
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 1
 ; LENGTH: 177
 ; TYPE: DNA
 ; ORGANISM: Leiurus quinquestriatus
 US-10-614-934-1

Alignment Scores:
 Pred. No.: 0.645 Length: 177
 Score: 73.00 Matches: 14
 Percent Similarity: 45.00% Conservative: 4
 Best Local Similarity: 35.00% Mismatches: 22
 Query Match: 27.44% Indels: 0
 DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-1 (1-177)

QY 5 CysGlnGlyGlnlySthrIleaSntYrArgCysaanaenSerglyGluCysIleProHis 24
 Db 55 TGTAGTGAACCTGCACTCAATAGACGTAAAGATGTTTGCATCTCGTGAATGTGGAGAGCT 114

QY 25 CysIleArgIleTyraSntHrArgAlaAlaLysCysIleAenlySthrCysaSnCysTyr 44
 Db 115 TGCAGAAAAGTAACAGAGATCGGACAGAAAGAAATGCCAGAAATTAATCAATGTCGCTGTAT 174


```
Db      1263 AACATCTCTCCGTGATGATGATGATCAAGACATTTCACAGAAATGTTCCACGAGCGTGC 1322
Qy      42 AsnCysTyr 44
        |||:::
Db      1323 GGATGCCAT 1331

RESULT 14
US-10-425-115-38929
; Sequence 38929, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovall, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 38929
; LENGTH: 2525
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_135504C.1
US-10-425-115-38929

Alignment Scores:
Pred. No.:      31.8      Length:      2525
Score:          71.50     Matches:      15
Percent Similarity: 34.92%  Conservative: 7
Best Local Similarity: 23.81%  Mismatches: 18
Query Match:    26.88%     Indels:      23
DB:             20        Gaps:          1

US-10-614-934-14 (1-45) x US-10-425-115-38929 (1-2525)
Qy      5 CysGlnGlnIleValysIleAsnTyrArgCysAsnAsnSerGlyGluCysIleProHis 24
        |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1842 TGCAGAGCCAGAGGAGATGATTTCTGTCAACCCAGTGAAGCTCAATTTGTGAC 1901
Qy      25 Cys-----
        |||
Db      1902 TGCTGCGGCAAGTGTCAAGGCGCTCCCAAGAAATGATCAACCGGGTCCAGTGGCCGA 1961
Qy      26 -----IleArgIleTyrAsnThrArgAlaIalysCysIleAsnIleThrCys 41
        |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1962 GAACATCTCTCCGTCAGATGATGATCAAGACATTTCCACAGATGTTCCACGAGCGTGC 2021
Qy      42 AsnCysTyr 44
        |||:::
Db      2022 GGATGCCAT 2030

RESULT 15
US-10-044-359-17
; Sequence 17, Application US/10044359
; Publication No. US20020160454A1
; GENERAL INFORMATION:
; APPLICANT: Hertman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BBI367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
```

```
; SEQ ID NO 17
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Hottentotta judaica
US-10-044-359-17

Alignment Scores:
Pred. No.:      1.22      Length:      177
Score:          71.00     Matches:      13
Percent Similarity: 52.94%  Conservative: 5
Best Local Similarity: 38.24%  Mismatches: 16
Query Match:    26.69%     Indels:      0
DB:             13        Gaps:          0

US-10-614-934-14 (1-45) x US-10-044-359-17 (1-177)
Qy      11 IleAsnTyrArgCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsn 30
        |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      73 ATGACGTAATAATGATTTCTCTCAAGAAATGTTGATGCTTTAAAAAGTAACGGA 132
Qy      31 ThrArgAlaIalysCysIleAsnIleThrCysAsnCysTyr 44
        |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      133 CGTTTCAAGGAAATGCCAGAAATTAACATATGCTGCTTTAT 174

Search completed: August 19, 2005, 05:04:30
Job time : 628 secs
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